

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2006, 20:21:18 ; Search time 35 Seconds  
(without alignments)  
1334.167 Million cell updates/sec

Perfect score: 3502  
Sequence: 1 MRYVLTMKASVIMFLVL.....QYVRIIQTCTEPNSOPRN 678

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA New:\*

- 1: /EMC\_Celettera\_SIDS3/ptodata/1/pubppaa/US09\_NEW\_PUB pep:\*
- 2: /EMC\_Celettera\_SIDS3/ptodata/1/pubppaa/US06\_NEW\_PUB pep:\*
- 3: /EMC\_Celettera\_SIDS3/ptodata/1/pubppaa/US07\_NEW\_PUB pep:\*
- 4: /EMC\_Celettera\_SIDS3/ptodata/1/pubppaa/US08\_NEW\_PUB pep:\*
- 5: /EMC\_Celettera\_SIDS3/ptodata/1/pubppaa/US09\_NEW\_PUB pep:\*
- 6: /EMC\_Celettera\_SIDS3/ptodata/1/pubppaa/US10\_NEW\_PUB pep:\*
- 7: /EMC\_Celettera\_SIDS3/ptodata/1/pubppaa/US11\_NEW\_PUB pep:\*
- 8: /EMC\_Celettera\_SIDS3/ptodata/1/pubppaa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	ID	Description
2	3502	100.0	678	US-11-101-316-34	Sequence 34, App1
3	3502	100.0	678	US-11-376-673-34	Sequence 34, App1
5	471.5	13.5	3176	US-11-105-233-155	Sequence 155, App1
6	357.5	10.2	956	US-10-527-101-8	Sequence 8, App1
7	325.5	9.3	732	US-11-274-634-14	Sequence 14, App1
8	324.5	9.3	732	US-11-274-634-14	Sequence 3, App1
9	282.5	8.1	488	US-11-274-634-14	Sequence 21, App1
10	270.5	7.7	2804	US-10-541-708-68	Sequence 48, App1
11	266	7.6	2813	US-11-222-346A-7	Sequence 21, App1
12	232	6.6	1152	US-09-970-076-3	Sequence 3, App1
13	231	6.6	1152	US-10-511-937-2444	Sequence 2444, App1
14	227.5	6.5	445	US-10-530-187-280	Sequence 280, App1
15	204.5	5.8	436	US-10-505-928-592	Sequence 592, App1
16	203.5	5.8	1170	US-10-511-937-8007	Sequence 3007, App1
17	193	5.5	1151	US-11-246-999-103	Sequence 103, App1
18	192.5	5.5	1034	US-11-246-999-43	Sequence 43, App1
19	192.5	5.5	1141	US-11-175-714-150	Sequence 150, App1
20	192.5	5.5	1166	US-11-175-714-148	Sequence 148, App1
21	192.5	5.5	1188	US-11-175-714-147	Sequence 147, App1
22	192.5	5.5	1189	US-11-246-999-35	Sequence 35, App1
23	191.5	5.5	1141	US-11-175-714-168	Sequence 168, App1
24	191.5	5.5	1166	US-11-175-714-166	Sequence 166, App1
25	191.5	5.5	1188	US-11-175-714-165	Sequence 165, App1
26	190.5	5.4	437	US-11-293-697-3386	Sequence 3386, App1
27	172	4.9	182	US-11-175-714-151	Sequence 151, App1
28	171	4.9	182	US-11-175-714-169	Sequence 169, App1

29	171	4.9	734	US-11-165-586-45	Sequence 45, App1
30	170.5	4.9	198	US-09-970-076-4	Sequence 4, App1
31	163.5	4.7	765	US-11-165-586-36	Sequence 36, App1
32	155.5	4.4	769	US-11-165-586-27	Sequence 27, App1
33	149.5	4.3	1132	US-11-347-179-5	Sequence 5, App1
34	149.5	4.3	1167	US-11-175-714-162	Sequence 162, App1
35	149.5	4.3	1167	US-11-347-179-4	Sequence 4, App1
37	134.5	3.8	485	US-11-056-355B-12397	Sequence 12397, A
38	133.5	3.8	213	US-11-222-346A-4	Sequence 4, App1
39	133.5	3.8	524	US-11-293-697-3442	Sequence 3442, App1
40	131.5	3.8	246	US-11-222-346A-5	Sequence 5, App1
41	131.5	3.8	247	US-11-350-353-4	Sequence 4, App1
42	127	3.6	419	US-11-056-355B-4A5520	Sequence 4A5520, A
43	119.5	3.4	213	US-11-222-346A-6	Sequence 6, App1
44	119.5	3.4	22152	US-10-544-944-1	Sequence 1, App1
45	116.5	3.3	2186	US-10-471-571A-860	Sequence 860, App1
46	115	3.3	375	US-11-056-355B-4A5521	Sequence 4A5521, A
47	114	3.3	571	US-10-449-902-42330	Sequence 42330, A
48	113.5	3.2	405	US-10-953-349-1810	Sequence 1810, App
49	113.5	3.2	413	US-10-953-349-1809	Sequence 1809, App
50	113.5	3.2	422	US-10-953-349-1808	Sequence 1808, App
51	113.5	3.2	480	US-10-374-780A-2902	Sequence 2902, App
52	112.5	3.2	748	US-10-449-902-42316	Sequence 42316, A
53	112	3.2	231	US-11-293-697-4167	Sequence 4167, App
54	111.5	3.2	382	US-10-953-349-24980	Sequence 24980, A
55	110.5	3.2	382	US-11-056-355B-54473	Sequence 54473, A
56	110.5	3.2	513	US-11-056-355B-78731	Sequence 78731, A
57	110	3.1	352	US-10-953-349-5351	Sequence 5351, App
58	110	3.1	352	US-10-953-349-5350	Sequence 5350, App
59	110	3.1	478	US-11-056-355B-78732	Sequence 78732, A
60	110	3.1	7632	US-10-374-780A-1433	Sequence 1433, App
61	109.5	3.1	2362	US-11-330-403-9773	Sequence 9773, App
62	109	3.1	345	US-11-330-403-17045	Sequence 17045, A
63	108.5	3.1	384	US-10-449-902-41009	Sequence 41009, A
64	108.5	3.1	681	US-10-953-349-10919	Sequence 10919, A
65	108.5	3.1	681	US-11-056-355B-45477	Sequence 45477, A
66	108.5	3.1	681	US-11-056-355B-49007	Sequence 49007, A
67	108	3.1	422	US-10-953-349-26025	Sequence 26025, A
68	108	3.1	422	US-11-056-355B-63446	Sequence 63446, A
69	107.5	3.1	666	US-10-449-902-45873	Sequence 45873, A
70	107.5	3.1	1055	US-10-449-902-45573	Sequence 45573, A
71	107.5	3.1	1058	US-10-449-902-31441	Sequence 31441, A
72	107	3.1	347	US-10-953-349-6391	Sequence 6391, App
73	106.5	3.0	380	US-11-056-355B-4A5522	Sequence 4A5522, A
74	106	3.0	1055	US-10-449-902-41244	Sequence 41244, A
75	105.5	3.0	684	US-10-449-902-45113	Sequence 45113, A
76	105	3.0	354	US-10-953-349-28519	Sequence 28519, A
77	105	3.0	354	US-11-056-355B-65407	Sequence 65407, A
78	104.5	3.0	2801	US-10-540-898-630	Sequence 630, App
79	104	3.0	493	US-11-056-355B-65494	Sequence 65494, A
80	103.5	3.0	509	US-11-056-355B-72369	Sequence 72369, A
81	103.5	3.0	533	US-11-174-307B-4904	Sequence 4904, App
82	103.5	3.0	533	US-11-293-697-3929	Sequence 3929, App
83	103.5	3.0	654	US-11-192-046-231	Sequence 231, App
84	103	2.9	334	US-11-293-697-2527	Sequence 2527, App
85	103	2.9	474	US-11-056-355B-72370	Sequence 72370, A
86	102.5	2.9	348	US-11-056-355B-8475	Sequence 8475, App
87	102.5	2.9	348	US-11-056-355B-13644	Sequence 13644, A
88	102.5	2.9	833	US-11-043-842-489	Sequence 489, App
89	102.5	2.9	833	US-11-043-842-502	Sequence 502, App
90	102.5	2.9	887	US-11-043-842-488	Sequence 488, App
91	102.5	2.9	940	US-10-449-902-44369	Sequence 44369, A
92	102.5	2.9	1084	US-11-043-842-490	Sequence 490, App
93	102.5	2.9	1253	US-11-043-842-491	Sequence 491, App
94	102.5	2.9	1339	US-11-043-842-494	Sequence 494, App
95	102.5	2.9	1337	US-11-043-842-491	Sequence 491, App
96	102.5	2.9	1415	US-11-043-842-492	Sequence 492, App
97	102.5	2.9	1463	US-11-043-842-493	Sequence 493, App
98	102.5	2.9	1533	US-11-043-842-495	Sequence 495, App
99	102.5	2.9	1533	US-11-043-842-505	Sequence 505, App
100	102.5	2.9	1555	US-11-043-842-506	Sequence 506, App
101	102.5	2.9	1579	US-11-043-842-498	Sequence 498, App
102	102.5	2.9	1657	US-11-043-842-499	Sequence 499, App

103	102.5	2.9	1670	7	US-11-043-842-496	Sequence 496, App	176	97	2.8	401.6	6	US-10-953-349-32548	Sequence 32548, A
104	102.5	2.9	1685	7	US-11-043-842-497	Sequence 497, App	177	97	2.8	512.7	7	US-11-056-355B-12249	Sequence 12249, A
105	102.5	2.9	1691	7	US-11-043-842-500	Sequence 500, App	178	97	2.8	587.7	7	US-11-293-697-3807	Sequence 3807, Ap
106	102.5	2.9	1744	6	US-10-530-187-199	Sequence 199, App	179	97	2.8	613.6	6	US-10-449-902-54118	Sequence 54118, A
107	102.5	2.9	1744	6	US-11-043-842-485	Sequence 485, App	180	97	2.8	897.7	7	US-11-330-403-2599	Sequence 2599, Ap
108	102.5	2.9	1744	7	US-11-043-842-486	Sequence 486, App	181	97	2.8	892.6	6	US-10-449-902-47486	Sequence 47486, A
109	102.5	2.9	1744	7	US-11-043-842-487	Sequence 487, App	182	97	2.8	293.3	6	US-10-953-349-31470	Sequence 31470, A
110	102	2.9	409	6	US-10-953-349-32547	Sequence 32547, A	183	96.5	2.8	315.7	7	US-11-056-355B-3593	Sequence 3693, Ap
111	102	2.9	432	6	US-10-449-902-56608	Sequence 56608, A	184	96.5	2.8	334.7	7	US-11-056-355B-11283	Sequence 16283, A
112	102	2.9	541	6	US-10-449-902-38744	Sequence 38744, A	185	96.5	2.8	330.7	7	US-11-330-403-31578	Sequence 11578, A
113	102	2.9	652	6	US-10-953-349-5551	Sequence 5551, Ap	186	96.5	2.8	513.7	6	US-11-330-403-31599	Sequence 11599, A
114	102	2.9	652	7	US-11-056-355B-30482	Sequence 30482, A	187	96.5	2.8	624.6	7	US-10-449-902-54592	Sequence 54592, A
115	102	2.9	652	7	US-11-056-355B-34072	Sequence 34072, A	188	96.5	2.8	773.3	6	US-10-953-349-2004	Sequence 2004, Ap
116	102	2.9	652	7	US-11-056-355B-97017	Sequence 97017, A	189	96.5	2.8	773.7	7	US-11-056-355B-42029	Sequence 42029, A
117	102	2.9	693	7	US-11-293-697-3849	Sequence 3849, Ap	190	96.5	2.8	773.7	7	US-11-056-355B-49630	Sequence 49630, A
118	101.5	2.9	580	6	US-10-449-902-46955	Sequence 46955, A	191	96.5	2.8	773.7	7	US-11-056-355B-104802	Sequence 104802, A
119	101.5	2.9	921	6	US-10-449-902-41147	Sequence 41147, A	192	96.5	2.8	773.7	7	US-11-056-355B-116041	Sequence 116041, A
120	101	2.9	326	6	US-10-953-349-17338	Sequence 17338, A	193	96.5	2.8	849.6	6	US-10-449-902-43302	Sequence 43302, A
121	101	2.9	326	7	US-11-056-355B-53421	Sequence 53421, A	194	96.5	2.8	851.6	6	US-10-953-349-11809	Sequence 11809, A
122	101	2.9	343	6	US-10-953-349-17337	Sequence 17337, A	195	96.5	2.8	887.6	6	US-10-953-349-11808	Sequence 11808, A
123	101	2.9	343	6	US-11-056-355B-53420	Sequence 53420, A	196	96.5	2.8	1004.6	6	US-10-953-349-11807	Sequence 11807, A
124	101	2.9	350	6	US-10-953-349-17336	Sequence 17336, A	197	96	2.7	332.7	7	US-11-330-403-31432	Sequence 31432, Ap
125	101	2.9	350	7	US-11-056-355B-53419	Sequence 53419, A	198	96	2.7	406.6	6	US-10-953-349-31643	Sequence 31643, A
126	101	2.9	392	6	US-10-449-902-56013	Sequence 56013, A	199	96	2.7	406.7	6	US-11-056-355B-68135	Sequence 68135, A
127	100.5	2.9	314	7	US-11-293-697-2665	Sequence 2665, Ap	200	96	2.7	418.6	7	US-10-449-902-41869	Sequence 41869, A
128	100.5	2.9	456	7	US-11-330-403-3246	Sequence 3246, Ap	201	96	2.7	558	6	US-10-449-902-55220	Sequence 55220, A
129	100.5	2.9	583	7	US-11-330-403-1250	Sequence 1250, Ap	202	96	2.7	559.7	7	US-11-330-403-11555	Sequence 11555, A
130	100.5	2.9	723	6	US-10-449-902-50323	Sequence 50323, A	203	96	2.7	583.7	7	US-11-330-403-9717	Sequence 9717, Ap
131	100.5	2.9	769	6	US-10-522-043-9	Sequence 9, Appli	204	96	2.7	796.6	7	US-10-449-902-52704	Sequence 52704, A
132	100	2.9	333	1	US-09-970-076-8	Sequence 8, Appli	205	96	2.7	819.6	6	US-10-449-902-41428	Sequence 41428, A
133	100	2.9	368	1	US-09-970-076-2	Sequence 2, Appli	206	96	2.7	1135.7	6	US-11-352-276-152	Sequence 152, App
134	100	2.9	494	7	US-11-330-403-1514	Sequence 1514, Ap	207	96	2.7	1384.6	6	US-10-505-928-799	Sequence 799, App
135	100	2.9	564	1	US-09-970-076-6	Sequence 6, Appli	208	96	2.7	1601.6	6	US-10-539-228-225	Sequence 225, App
136	100	2.9	791	6	US-10-449-902-51140	Sequence 51140, A	209	96	2.7	2160.7	6	US-11-252-276-22	Sequence 22, Appl
137	100	2.9	791	6	US-10-449-902-53452	Sequence 53452, A	210	96	2.7	436.4	7	US-11-374-683-14	Sequence 14, Appl
138	99.5	2.8	350	6	US-11-330-403-44784	Sequence 44784, A	211	95.5	2.7	336.6	6	US-10-449-902-37556	Sequence 3756, A
139	99.5	2.8	411	6	US-10-449-902-8078	Sequence 8078, A	212	95.5	2.7	443.6	6	US-10-449-902-28738	Sequence 2878, A
140	99.5	2.8	915	6	US-10-523-014-4	Sequence 4, Appli	213	95.5	2.7	541.7	7	US-11-056-355B-12032	Sequence 12032, A
141	99	2.8	335	6	US-10-953-349-25256	Sequence 25256, A	214	95.5	2.7	782.6	6	US-10-539-228-438	Sequence 438, A
142	99	2.8	338	6	US-10-953-349-24981	Sequence 24981, A	215	95.5	2.7	1217.7	7	US-11-105-233-186	Sequence 186, App
143	99	2.8	338	7	US-11-056-355B-54474	Sequence 54474, A	216	95	2.7	282.7	7	US-11-056-355B-55443	Sequence 5643, Ap
144	99	2.8	384	6	US-10-505-928-395	Sequence 395, App	217	95	2.7	654.6	6	US-10-480-962-9	Sequence 9, Appli
145	99	2.8	535	6	US-10-449-902-45610	Sequence 45610, A	218	95	2.7	756.6	6	US-10-527-572-6	Sequence 6, Appli
146	99	2.8	632	7	US-11-056-355B-45762	Sequence 45762, A	219	95	2.7	2829.6	6	US-10-525-621-1	Sequence 1, Appli
147	99	2.8	642	6	US-10-449-902-38761	Sequence 38761, A	220	94.5	2.7	289.7	7	US-11-056-355B-11207	Sequence 13207, A
148	99	2.8	759	6	US-10-449-902-41321	Sequence 41321, A	221	94.5	2.7	289.7	7	US-11-321-421-92	Sequence 92, Appl
149	99	2.8	856	6	US-10-449-902-41385	Sequence 41385, A	222	94.5	2.7	334.6	6	US-10-540-898-92	Sequence 92, Appl
150	98.5	2.8	661	7	US-11-031-338A-2	Sequence 2, Appli	223	94.5	2.7	448.7	7	US-11-056-355B-50507	Sequence 50507, A
151	98.5	2.8	661	7	US-11-323-964-13	Sequence 13, Appli	224	94.5	2.7	448.7	7	US-11-056-355B-50506	Sequence 50506, A
152	98.5	2.8	1040	6	US-10-449-902-41183	Sequence 41183, A	225	94.5	2.7	447.7	7	US-11-056-355B-102293	Sequence 102293, A
153	98.5	2.8	1744	6	US-10-530-187-200	Sequence 200, App	226	94.5	2.7	447.7	7	US-11-056-355B-113532	Sequence 113532, A
154	98.5	2.8	4373	7	US-11-118-524-2	Sequence 2, Appli	227	94.5	2.7	571.7	7	US-11-330-403-5559	Sequence 5559, Ap
155	98	2.8	375	7	US-11-056-355B-19619	Sequence 19619, A	228	94.5	2.7	571.7	7	US-11-056-355B-50505	Sequence 50505, A
156	98	2.8	392	7	US-11-192-046-40	Sequence 40, Appl	229	94.5	2.7	572.6	6	US-10-449-902-36166	Sequence 36166, A
157	98	2.8	432	7	US-11-192-046-39	Sequence 39, Appl	230	94.5	2.7	572.6	6	US-10-449-902-52883	Sequence 52883, A
158	98	2.8	559	6	US-10-449-902-33440	Sequence 33440, A	231	94.5	2.7	572.6	6	US-10-449-902-53440	Sequence 53440, A
159	98	2.8	878	6	US-10-449-902-41180	Sequence 41180, A	232	94.5	2.7	575.7	7	US-11-301-457-17	Sequence 17, Appl
160	98	2.8	1078	6	US-10-449-902-54534	Sequence 54534, A	233	94.5	2.7	604.7	7	US-11-056-355B-79157	Sequence 79157, A
161	98	2.8	9535	6	US-10-471-571A-4496	Sequence 4496, Ap	234	94.5	2.7	606.7	6	US-11-056-355B-79156	Sequence 79156, A
162	97.5	2.8	222	6	US-10-953-349-27868	Sequence 27868, A	235	94.5	2.7	713.6	6	US-10-471-571A-4732	Sequence 4732, Ap
163	97.5	2.8	222	7	US-11-056-355B-65337	Sequence 65337, A	236	94.5	2.7	717.7	7	US-11-056-355B-79155	Sequence 79155, A
164	97.5	2.8	745	6	US-10-449-902-38719	Sequence 38719, A	237	94.5	2.7	802.6	6	US-10-527-572-5	Sequence 5, Appli
165	97.5	2.8	745	6	US-11-293-697-4038	Sequence 4038, Ap	238	94.5	2.7	802.6	6	US-10-449-902-46790	Sequence 46790, A
166	97.5	2.8	785	6	US-10-953-349-3003	Sequence 3003, Ap	239	94.5	2.7	837.7	7	US-11-330-403-19064	Sequence 19064, A
167	97.5	2.8	785	7	US-11-056-355B-42028	Sequence 42028, Ap	240	94.5	2.7	1089.7	6	US-10-449-902-48650	Sequence 48650, A
168	97.5	2.8	785	7	US-11-056-355B-49629	Sequence 49629, A	241	94.5	2.7	1306.7	7	US-11-351-208-6	Sequence 6, Appli
169	97.5	2.8	785	7	US-11-056-355B-104801	Sequence 104801, A	242	94	2.7	214.6	6	US-10-953-349-39381	Sequence 39381, A
170	97.5	2.8	785	7	US-11-056-355B-116040	Sequence 116040, A	243	94	2.7	214.6	6	US-11-056-355B-1364	Sequence 1364, Ap
171	97.5	2.8	926	7	US-11-056-355B-71218	Sequence 71218, A	244	94	2.7	367.7	6	US-10-953-349-26027	Sequence 26027, A
172	97.5	2.8	1129	7	US-11-330-403-16432	Sequence 16432, A	245	94	2.7	367.7	6	US-11-056-355B-63448	Sequence 63448, A
173	97.5	2.8	1194	6	US-10-449-902-41263	Sequence 41263, A	246	94	2.7	368.6	6	US-10-953-349-26026	Sequence 26026, A
174	97.5	2.8	1434	6	US-11-192-046-36	Sequence 36, Appl	247	94	2.7	368.7	6	US-11-056-355B-63447	Sequence 63447, A
175	97	2.8	400	6	US-10-953-349-32549	Sequence 32549, A	248	94	2.7	513.7	7	US-11-330-403-6712	Sequence 6712, Ap

249	94	2.7	1016	6	US-10-449-902-43402	Sequence 43402, A	322	91	2.6	353	7	US-11-271-287-33	Sequence 33, Appl
250	94	2.7	1471	7	US-11-330-403-14431	Sequence 14431, A	323	91	2.6	373	6	US-10-953-349-11149	Sequence 31149, A
251	93.5	2.7	514	6	US-10-449-902-50931	Sequence 50931, A	324	91	2.6	380	7	US-11-056-355B-2695	Sequence 2695, Ap
252	93.5	2.7	548	6	US-10-449-902-29496	Sequence 29496, A	325	91	2.6	488	7	US-11-330-403-18128	Sequence 18128, A
253	93.5	2.7	585	6	US-10-449-902-53167	Sequence 53167, A	326	91	2.6	626	7	US-11-358-419-413	Sequence 413, Appl
254	93.5	2.7	595	7	US-11-056-355B-83512	Sequence 83512, A	327	91	2.6	626	7	US-11-378-923-23	Sequence 23, Appl
255	93.5	2.7	598	7	US-11-056-355B-83511	Sequence 83511, A	328	91	2.6	626	7	US-11-378-923-24	Sequence 24, Appl
256	93.5	2.7	617	6	US-10-449-902-36554	Sequence 36554, A	329	91	2.6	691	7	US-11-056-355B-79590	Sequence 79590, A
257	93.5	2.7	764	6	US-10-449-902-46298	Sequence 46298, A	330	91	2.6	698	6	US-10-449-902-53993	Sequence 53993, A
258	93.5	2.7	905	6	US-10-449-902-41605	Sequence 41605, A	331	91	2.6	712	7	US-11-105-233-162	Sequence 162, App
259	93.5	2.7	918	7	US-11-056-355B-78379	Sequence 78379, A	332	91	2.6	712	7	US-11-121-133-262	Sequence 262, App
260	93.5	2.7	1127	6	US-10-449-902-53809	Sequence 53809, A	333	91	2.6	712	7	US-11-121-133-263	Sequence 263, App
261	93.5	2.7	2240	6	US-10-544-731-4	Sequence 4, Appl1	334	91	2.6	712	7	US-11-121-133-264	Sequence 264, App
262	93.5	2.7	2258	6	US-10-544-731-3	Sequence 3, Appl1	335	91	2.6	718	7	US-11-056-355B-79589	Sequence 79589, A
263	93.5	2.7	2264	6	US-10-544-731-5	Sequence 5, Appl1	336	91	2.6	847	7	US-11-056-355B-79588	Sequence 79588, A
264	93	2.7	251	6	US-10-953-349-9196	Sequence 9196, Ap	337	91	2.6	883	7	US-11-192-046-188	Sequence 188, App
265	93	2.7	251	7	US-11-056-355B-39265	Sequence 39265, A	338	91	2.6	883	7	US-11-192-046-195	Sequence 195, App
266	93	2.7	251	7	US-11-056-355B-41773	Sequence 41773, A	339	91	2.6	883	7	US-11-192-046-202	Sequence 202, App
267	93	2.7	302	6	US-10-953-349-9195	Sequence 9195, Ap	340	91	2.6	883	7	US-11-192-046-216	Sequence 216, App
268	93	2.7	302	6	US-11-056-355B-39264	Sequence 39264, A	341	91	2.6	883	7	US-11-192-046-237	Sequence 237, App
269	93	2.7	302	7	US-11-056-355B-41772	Sequence 41772, A	342	91	2.6	890	7	US-11-192-046-173	Sequence 173, Appl
270	93	2.7	326	6	US-10-953-349-9194	Sequence 9194, Ap	343	91	2.6	1226	7	US-11-221-332-88	Sequence 88, Appl
271	93	2.7	326	7	US-11-056-355B-39263	Sequence 39263, A	344	90.5	2.6	1227	7	US-11-056-355B-113708	Sequence 13708, A
272	93	2.7	326	7	US-11-056-355B-41771	Sequence 41771, A	345	90.5	2.6	1227	7	US-10-449-902-33415	Sequence 33415, A
273	93	2.7	361	7	US-11-056-355B-1150	Sequence 1150, Ap	346	90.5	2.6	1227	7	US-10-449-902-42619	Sequence 42619, A
274	93	2.7	381	7	US-11-056-355B-1149	Sequence 1149, Ap	347	90.5	2.6	1227	7	US-11-330-403-13209	Sequence 13209, A
275	93	2.7	594	6	US-10-449-902-47022	Sequence 47022, A	348	90.5	2.6	500	7	US-10-449-902-47505	Sequence 47505, A
276	93	2.7	594	6	US-10-449-902-52090	Sequence 52090, A	349	90.5	2.6	521	6	US-10-449-902-54672	Sequence 54672, A
277	93	2.7	627	7	US-11-358-419-47	Sequence 47, Appl	350	90.5	2.6	570	6	US-10-449-902-51709	Sequence 51709, A
278	93	2.7	657	6	US-10-449-902-41222	Sequence 41222, A	351	90.5	2.6	579	6	US-10-449-902-52147	Sequence 52147, A
279	93	2.7	879	6	US-10-540-898-258	Sequence 258, App	352	90.5	2.6	627	6	US-10-449-902-45456	Sequence 45456, A
280	93	2.7	901	6	US-10-540-898-870	Sequence 870, App	353	90.5	2.6	634	6	US-10-449-902-55716	Sequence 55716, A
281	93	2.7	1786	6	US-10-519-328-2	Sequence 2, Appl1	354	90.5	2.6	710	6	US-10-449-902-41319	Sequence 41319, A
282	93	2.7	1821	6	US-10-505-928-451	Sequence 451, App	355	90.5	2.6	727	6	US-10-449-902-53529	Sequence 53529, A
283	93	2.7	1821	6	US-10-519-328-1	Sequence 1, Appl1	356	90.5	2.6	866	6	US-10-449-902-41251	Sequence 41251, A
284	92.5	2.6	202	7	US-11-056-355B-52874	Sequence 52874, A	357	90.5	2.6	888	7	US-11-056-355B-75789	Sequence 75789, A
285	92.5	2.6	334	6	US-10-449-902-0166	Sequence 40166, A	358	90.5	2.6	882	6	US-10-977-350-4	Sequence 4, Appl1
286	92.5	2.6	334	6	US-11-349-852-7	Sequence 7, Appl1	359	90.5	2.6	929	6	US-10-449-902-41088	Sequence 41088, A
287	92.5	2.6	342	6	US-10-449-902-9563	Sequence 49563, A	360	90.5	2.6	1073	6	US-10-449-902-41088	Sequence 41088, A
288	92.5	2.6	359	7	US-11-349-852-8	Sequence 8, Appl1	361	90.5	2.6	1122	6	US-10-540-898-260	Sequence 260, App
289	92.5	2.6	364	6	US-10-505-928-605	Sequence 605, Appl1	362	90.5	2.6	1433	7	US-11-330-403-8279	Sequence 8279, App
290	92.5	2.6	382	7	US-11-293-697-6654	Sequence 3654, App	363	90.5	2.6	1572	7	US-11-330-403-12338	Sequence 12338, A
291	92.5	2.6	505	7	US-11-330-403-18387	Sequence 18387, A	364	90	2.6	302	7	US-11-056-355B-8476	Sequence 8476, Ap
292	92.5	2.6	590	6	US-10-449-902-55352	Sequence 55352, A	365	90	2.6	302	7	US-11-056-355B-15645	Sequence 13645, A
293	92.5	2.6	861	7	US-11-293-431-3	Sequence 3, Appl1	366	90	2.6	302	7	US-11-056-355B-16284	Sequence 16284, A
294	92.5	2.6	907	7	US-11-293-697-2845	Sequence 2845, Ap	367	90	2.6	317	6	US-10-953-349-17089	Sequence 17089, A
295	92.5	2.6	1017	6	US-10-449-902-41143	Sequence 41143, A	368	90	2.6	339	6	US-10-953-349-17088	Sequence 17088, A
296	92.5	2.6	2828	6	US-10-700-439-124	Sequence 124, App	369	90	2.6	347	6	US-10-953-349-17087	Sequence 17087, A
297	92	2.6	245	6	US-10-449-902-8546	Sequence 38546, A	370	90	2.6	412	7	US-11-056-355B-8069	Sequence 8069, Ap
298	92	2.6	315	7	US-11-056-355B-63975	Sequence 63975, A	371	90	2.6	557	6	US-10-449-902-28939	Sequence 28939, A
299	92	2.6	427	6	US-10-449-902-53158	Sequence 53158, A	372	90	2.6	587	7	US-11-056-355B-107995	Sequence 107995, A
300	92	2.6	561	6	US-11-330-403-12349	Sequence 12349, A	373	90	2.6	587	7	US-11-056-355B-119234	Sequence 119234, A
301	92	2.6	597	6	US-10-953-349-5074	Sequence 5074, Ap	374	90	2.6	719	7	US-11-056-355B-179394	Sequence 179394, A
302	92	2.6	648	6	US-10-449-902-36823	Sequence 36823, A	375	90	2.6	719	7	US-11-056-355B-119233	Sequence 119233, A
303	92	2.6	675	6	US-10-449-902-84447	Sequence 48447, A	376	90	2.6	877	7	US-11-056-355B-35835	Sequence 35835, A
304	92	2.6	675	6	US-10-449-902-50618	Sequence 50618, A	377	90	2.6	877	7	US-11-056-355B-44815	Sequence 44815, A
305	92	2.6	709	6	US-10-449-902-52735	Sequence 52735, A	378	90	2.6	885	7	US-11-056-355B-39834	Sequence 39834, A
306	92	2.6	712	6	US-10-530-187-296	Sequence 296, App	379	90	2.6	885	7	US-11-056-355B-44814	Sequence 44814, A
307	92	2.6	1123	7	US-11-330-403-11476	Sequence 11476, A	380	90	2.6	918	6	US-10-449-902-41221	Sequence 41221, A
308	92	2.6	1123	7	US-11-330-403-15911	Sequence 15911, A	381	90	2.6	918	6	US-11-056-355B-35833	Sequence 35833, A
309	92	2.6	1123	7	US-11-330-403-15911	Sequence 15911, A	382	90	2.6	918	6	US-11-056-355B-44813	Sequence 44813, A
310	92	2.6	1135	7	US-11-301-457-21	Sequence 21, Appl1	383	90	2.6	968	6	US-10-449-902-41123	Sequence 41123, A
311	92	2.6	1581	7	US-11-283-329-162	Sequence 162, App	384	90	2.6	985	7	US-11-442-171-6	Sequence 6, Appl1
312	91.5	2.6	317	7	US-11-056-355B-68675	Sequence 68675, A	385	90	2.6	985	7	US-11-442-171-66	Sequence 66, Appl1
313	91.5	2.6	359	7	US-11-056-355B-68674	Sequence 68674, A	386	90	2.6	1123	7	US-11-330-403-17347	Sequence 17347, A
314	91.5	2.6	359	7	US-11-330-403-13146	Sequence 3146, Ap	387	90	2.6	1704	7	US-11-250-089-40	Sequence 40, Appl1
315	91.5	2.6	423	7	US-11-056-355B-68673	Sequence 68673, A	388	90	2.6	310	6	US-10-953-349-24982	Sequence 24982, A
316	91.5	2.6	718	7	US-11-056-355B-79095	Sequence 79095, A	389	89.5	2.6	310	6	US-11-056-355B-54475	Sequence 54475, A
317	91.5	2.6	940	6	US-10-449-902-14146	Sequence 14146, A	390	89.5	2.6	317	7	US-11-056-355B-50674	Sequence 50674, A
318	91.5	2.6	957	6	US-11-330-403-9644	Sequence 9644, Ap	391	89.5	2.6	372	7	US-11-056-355B-50673	Sequence 50673, A
319	91	2.6	214	6	US-10-449-902-55454	Sequence 55454, A	392	89.5	2.6	434	6	US-10-449-902-50843	Sequence 50843, A
320	91	2.6	251	6	US-11-284-236-212	Sequence 212, App	393	89.5	2.6	438	6	US-10-953-349-11788	Sequence 11788, A
321	91	2.6	344	7	US-11-121-133-173	Sequence 173, App	394	89.5	2.6	438	7	US-11-056-355B-48934	Sequence 48934, A

395	89.5	2.6	440	6	US-10-953-349-11277	Sequence 11277, A	468	89.5	2.6	499	7	US-11-241-596-230	Sequence 230, App
396	89.5	2.6	440	7	US-11-056-355B-48933	Sequence 48933, A	469	89.5	2.6	499	7	US-11-241-596-231	Sequence 231, App
397	89.5	2.6	499	7	US-11-241-596-159	Sequence 159, App	470	89.5	2.6	499	7	US-11-241-596-232	Sequence 232, App
398	89.5	2.6	499	7	US-11-241-596-160	Sequence 160, App	471	89.5	2.6	499	7	US-11-241-596-233	Sequence 233, App
399	89.5	2.6	499	7	US-11-241-596-161	Sequence 161, App	472	89.5	2.6	499	7	US-11-241-596-234	Sequence 234, App
400	89.5	2.6	499	7	US-11-241-596-162	Sequence 162, App	473	89.5	2.6	499	7	US-11-241-596-235	Sequence 235, App
401	89.5	2.6	499	7	US-11-241-596-163	Sequence 163, App	474	89.5	2.6	499	7	US-11-241-596-236	Sequence 236, App
402	89.5	2.6	499	7	US-11-241-596-164	Sequence 164, App	475	89.5	2.6	499	7	US-11-241-596-237	Sequence 237, App
403	89.5	2.6	499	7	US-11-241-596-165	Sequence 165, App	476	89.5	2.6	499	7	US-11-241-596-238	Sequence 238, App
404	89.5	2.6	499	7	US-11-241-596-166	Sequence 166, App	477	89.5	2.6	499	7	US-11-241-596-239	Sequence 239, App
405	89.5	2.6	499	7	US-11-241-596-167	Sequence 167, App	478	89.5	2.6	499	7	US-11-241-596-240	Sequence 240, App
406	89.5	2.6	499	7	US-11-241-596-168	Sequence 168, App	479	89.5	2.6	499	7	US-11-241-596-241	Sequence 241, App
407	89.5	2.6	499	7	US-11-241-596-169	Sequence 169, App	480	89.5	2.6	499	7	US-11-241-596-242	Sequence 242, App
408	89.5	2.6	499	7	US-11-241-596-170	Sequence 170, App	481	89.5	2.6	499	7	US-11-241-596-243	Sequence 243, App
409	89.5	2.6	499	7	US-11-241-596-171	Sequence 171, App	482	89.5	2.6	499	7	US-11-241-596-244	Sequence 244, App
410	89.5	2.6	499	7	US-11-241-596-172	Sequence 172, App	483	89.5	2.6	499	7	US-11-241-596-245	Sequence 245, App
411	89.5	2.6	499	7	US-11-241-596-173	Sequence 173, App	484	89.5	2.6	499	7	US-11-241-596-246	Sequence 246, App
412	89.5	2.6	499	7	US-11-241-596-174	Sequence 174, App	485	89.5	2.6	499	7	US-11-241-596-247	Sequence 247, App
413	89.5	2.6	499	7	US-11-241-596-175	Sequence 175, App	486	89.5	2.6	499	7	US-11-241-596-248	Sequence 248, App
414	89.5	2.6	499	7	US-11-241-596-176	Sequence 176, App	487	89.5	2.6	499	7	US-11-241-596-249	Sequence 249, App
415	89.5	2.6	499	7	US-11-241-596-177	Sequence 177, App	488	89.5	2.6	499	7	US-11-241-596-250	Sequence 250, App
416	89.5	2.6	499	7	US-11-241-596-178	Sequence 178, App	489	89.5	2.6	499	7	US-11-241-596-251	Sequence 251, App
417	89.5	2.6	499	7	US-11-241-596-179	Sequence 179, App	490	89.5	2.6	499	7	US-11-241-596-252	Sequence 252, App
418	89.5	2.6	499	7	US-11-241-596-180	Sequence 180, App	491	89.5	2.6	499	7	US-11-241-596-253	Sequence 253, App
419	89.5	2.6	499	7	US-11-241-596-181	Sequence 181, App	492	89.5	2.6	499	7	US-11-241-596-254	Sequence 254, App
420	89.5	2.6	499	7	US-11-241-596-182	Sequence 182, App	493	89.5	2.6	501	6	US-10-449-902-33237	Sequence 33237, A
421	89.5	2.6	499	7	US-11-241-596-183	Sequence 183, App	494	89.5	2.6	502	6	US-10-449-902-36747	Sequence 36747, A
422	89.5	2.6	499	7	US-11-241-596-184	Sequence 184, App	495	89.5	2.6	509	6	US-10-953-349-24078	Sequence 24078, A
423	89.5	2.6	499	7	US-11-241-596-185	Sequence 185, App	496	89.5	2.6	509	6	US-11-056-355B-57991	Sequence 57991, A
424	89.5	2.6	499	7	US-11-241-596-186	Sequence 186, App	497	89.5	2.6	516	6	US-10-953-349-24077	Sequence 24077, A
425	89.5	2.6	499	7	US-11-241-596-187	Sequence 187, App	498	89.5	2.6	516	6	US-11-056-355B-57990	Sequence 57990, A
426	89.5	2.6	499	7	US-11-241-596-188	Sequence 188, App	499	89.5	2.6	521	6	US-10-449-902-48426	Sequence 48426, A
427	89.5	2.6	499	7	US-11-241-596-189	Sequence 189, App	500	89.5	2.6	571	6	US-10-953-349-11876	Sequence 11876, A
428	89.5	2.6	499	7	US-11-241-596-190	Sequence 190, App	501	89.5	2.6	571	7	US-11-056-355B-44932	Sequence 44932, A
429	89.5	2.6	499	7	US-11-241-596-191	Sequence 191, App	502	89.5	2.6	594	7	US-11-330-403-1851	Sequence 1851, App
430	89.5	2.6	499	7	US-11-241-596-192	Sequence 192, App	503	89.5	2.6	643	6	US-10-505-928-248	Sequence 248, App
431	89.5	2.6	499	7	US-11-241-596-193	Sequence 193, App	504	89.5	2.6	617	7	US-11-293-697-4521	Sequence 4521, App
432	89.5	2.6	499	7	US-11-241-596-194	Sequence 194, App	505	89.5	2.6	1058	6	US-11-221-332-78	Sequence 332, App1
433	89.5	2.6	499	7	US-11-241-596-195	Sequence 195, App	507	89.5	2.6	1058	7	US-11-251-673-3	Sequence 3, App1
434	89.5	2.6	499	7	US-11-241-596-196	Sequence 196, App	508	89.5	2.6	1058	7	US-10-449-902-47933	Sequence 47933, A
435	89.5	2.6	499	7	US-11-241-596-197	Sequence 197, App	509	89.5	2.6	1105	6	US-10-449-902-41991	Sequence 41991, A
436	89.5	2.6	499	7	US-11-241-596-198	Sequence 198, App	510	89.5	2.6	1215	6	US-10-505-928-75	Sequence 75, App1
437	89.5	2.6	499	7	US-11-241-596-199	Sequence 199, App	511	89.5	2.6	1734	6	US-11-358-419-81	Sequence 81, App1
438	89.5	2.6	499	7	US-11-241-596-200	Sequence 200, App	512	89.5	2.6	1763	6	US-10-504-120-21	Sequence 21, App1
439	89.5	2.6	499	7	US-11-241-596-201	Sequence 201, App	513	89.5	2.6	1807	6	US-10-504-120-22	Sequence 22, App1
440	89.5	2.6	499	7	US-11-241-596-202	Sequence 202, App	514	89	2.5	227	6	US-10-953-349-32122	Sequence 32122, A
441	89.5	2.6	499	7	US-11-241-596-203	Sequence 203, App	515	89	2.5	242	6	US-10-953-349-34822	Sequence 34822, A
442	89.5	2.6	499	7	US-11-241-596-204	Sequence 204, App	516	89	2.5	242	7	US-11-056-355B-4824	Sequence 47824, App
443	89.5	2.6	499	7	US-11-241-596-205	Sequence 205, App	517	89	2.5	212	6	US-10-953-349-32121	Sequence 32121, A
444	89.5	2.6	499	7	US-11-241-596-206	Sequence 206, App	518	89	2.5	287	7	US-11-056-355B-71099	Sequence 71099, A
445	89.5	2.6	499	7	US-11-241-596-207	Sequence 207, App	519	89	2.5	370	7	US-11-056-355B-71098	Sequence 71098, A
446	89.5	2.6	499	7	US-11-241-596-208	Sequence 208, App	520	89	2.5	376	7	US-11-330-403-19136	Sequence 19136, A
447	89.5	2.6	499	7	US-11-241-596-209	Sequence 209, App	521	89	2.5	386	7	US-11-056-355B-71097	Sequence 71097, A
448	89.5	2.6	499	7	US-11-241-596-210	Sequence 210, App	522	89	2.5	412	7	US-11-056-355B-12553	Sequence 12553, A
449	89.5	2.6	499	7	US-11-241-596-211	Sequence 211, App	523	89	2.5	414	7	US-11-056-355B-6572	Sequence 6572, App
450	89.5	2.6	499	7	US-11-241-596-212	Sequence 212, App	524	89	2.5	537	6	US-10-953-349-4553	Sequence 4553, App
451	89.5	2.6	499	7	US-11-241-596-213	Sequence 213, App	525	89	2.5	537	7	US-11-056-355B-28387	Sequence 28387, A
452	89.5	2.6	499	7	US-11-241-596-214	Sequence 214, App	526	89	2.5	537	7	US-11-056-355B-31977	Sequence 31977, A
453	89.5	2.6	499	7	US-11-241-596-215	Sequence 215, App	527	89	2.5	537	7	US-11-056-355B-84465	Sequence 84465, A
454	89.5	2.6	499	7	US-11-241-596-216	Sequence 216, App	528	89	2.5	546	7	US-11-330-403-10163	Sequence 10163, A
455	89.5	2.6	499	7	US-11-241-596-217	Sequence 217, App	529	89	2.5	599	7	US-11-316-521-45	Sequence 45, App1
456	89.5	2.6	499	7	US-11-241-596-218	Sequence 218, App	530	89	2.5	559	7	US-11-330-403-1505	Sequence 1505, App
457	89.5	2.6	499	7	US-11-241-596-219	Sequence 219, App	531	89	2.5	559	7	US-11-330-403-2392	Sequence 2392, App
458	89.5	2.6	499	7	US-11-241-596-220	Sequence 220, App	532	89	2.5	559	7	US-11-330-403-9433	Sequence 9433, App
459	89.5	2.6	499	7	US-11-241-596-221	Sequence 221, App	533	89	2.5	559	7	US-11-330-403-9654	Sequence 9654, App
460	89.5	2.6	499	7	US-11-241-596-222	Sequence 222, App	534	89	2.5	560	7	US-11-330-403-14413	Sequence 14413, A
461	89.5	2.6	499	7	US-11-241-596-223	Sequence 223, App	535	89	2.5	563	7	US-11-330-403-3729	Sequence 3729, App
462	89.5	2.6	499	7	US-11-241-596-224	Sequence 224, App	536	89	2.5	595	6	US-10-449-902-38085	Sequence 38085, A
463	89.5	2.6	499	7	US-11-241-596-225	Sequence 225, App	537	89	2.5	602	6	US-10-953-349-4552	Sequence 4552, App
464	89.5	2.6	499	7	US-11-241-596-226	Sequence 226, App	538	89	2.5	602	7	US-11-056-355B-28386	Sequence 28386, A
465	89.5	2.6	499	7	US-11-241-596-227	Sequence 227, App	539	89	2.5	602	7	US-11-056-355B-31976	Sequence 31976, A
466	89.5	2.6	499	7	US-11-241-596-228	Sequence 228, App	540	89	2.5	602	7	US-11-056-355B-84464	Sequence 84464, A
467	89.5	2.6	499	7	US-11-241-596-229	Sequence 229, App	541	89	2.5	634	7	US-11-330-403-323	Sequence 323, App















1419 80 2.3 720 7 US-11-056-355B-18245  
1420 80 2.3 727 6 US-10-449-902-52923  
1421 80 2.3 732 7 US-11-056-355B-69970  
1422 80 2.3 749 7 US-11-056-355B-73156  
1423 80 2.3 788 6 US-10-449-902-54720  
1424 80 2.3 830 6 US-10-449-902-41209  
1425 80 2.3 838 6 US-10-449-902-45252  
1426 80 2.3 857 7 US-11-056-355B-70345  
1427 80 2.3 857 7 US-11-056-355B-87802  
1428 80 2.3 860 7 US-11-233-508-11  
1429 80 2.3 905 6 US-10-540-898-873  
1430 80 2.3 928 6 US-10-449-902-50474  
1431 80 2.3 931 7 US-11-056-355B-70344  
1432 80 2.3 931 7 US-11-056-355B-87801  
1433 80 2.3 972 7 US-11-330-403-15402  
1434 80 2.3 988 6 US-10-374-780A-238  
1435 80 2.3 1076 7 US-11-056-355B-70343  
1436 80 2.3 1076 7 US-11-056-355B-87800  
1437 80 2.3 1111 6 US-10-449-902-51182  
1438 80 2.3 1122 7 US-11-330-403-16478  
1439 80 2.3 1124 7 US-11-193-353-2  
1440 80 2.3 1131 7 US-11-330-403-17082  
1441 80 2.3 1136 7 US-11-330-403-14115  
1442 80 2.3 1224 6 US-10-449-902-11405  
1443 80 2.3 1390 6 US-10-449-902-41141  
1444 80 2.3 1478 7 US-11-330-403-16140  
1445 80 2.3 1478 7 US-11-330-403-16764  
1446 80 2.3 1565 7 US-11-330-403-6564  
1447 80 2.3 1595 6 US-10-486-020-18  
1448 80 2.3 1691 7 US-11-056-355B-104646  
1449 80 2.3 1691 7 US-11-056-355B-115885  
1450 80 2.3 1705 7 US-11-056-355B-104645  
1451 80 2.3 1705 7 US-11-056-355B-115884  
1452 80 2.3 1748 7 US-11-056-355B-104644  
1453 80 2.3 1748 7 US-11-056-355B-115883  
1454 80 2.3 2343 6 US-10-540-898-904  
1455 80 2.3 2511 7 US-11-051-725-12  
1456 80 2.3 2511 7 US-11-051-725-13  
1457 80 2.3 2523 7 US-11-051-725-11  
1458 79.5 2.3 177 7 US-11-056-355B-9410  
1459 79.5 2.3 206 7 US-11-056-355B-37391  
1460 79.5 2.3 229 6 US-10-953-349-35175  
1461 79.5 2.3 295 6 US-10-953-349-23990  
1462 79.5 2.3 295 6 US-11-056-355B-58004  
1463 79.5 2.3 297 6 US-10-953-349-14256  
1464 79.5 2.3 299 6 US-10-953-349-14255  
1465 79.5 2.3 300 6 US-10-953-349-23989  
1466 79.5 2.3 300 7 US-11-056-355B-58003  
1467 79.5 2.3 344 7 US-11-192-046-75  
1468 79.5 2.3 353 7 US-11-056-355B-2866  
1469 79.5 2.3 373 6 US-10-521-140-19  
1470 79.5 2.3 378 7 US-11-056-355B-40899  
1471 79.5 2.3 420 7 US-11-056-355B-49256  
1472 79.5 2.3 425 7 US-11-056-355B-50065  
1473 79.5 2.3 427 7 US-11-056-355B-14103  
1474 79.5 2.3 428 6 US-10-449-902-48982  
1475 79.5 2.3 433 6 US-10-449-902-38367  
1476 79.5 2.3 436 6 US-10-374-780A-32  
1477 79.5 2.3 441 7 US-11-289-102-368  
1478 79.5 2.3 447 6 US-10-449-902-39826  
1479 79.5 2.3 455 6 US-10-953-349-10318  
1480 79.5 2.3 460 7 US-11-056-355B-79755  
1481 79.5 2.3 463 6 US-10-449-902-42963  
1482 79.5 2.3 468 6 US-10-953-349-11424  
1483 79.5 2.3 471 7 US-11-293-697-2588  
1484 79.5 2.3 476 6 US-10-449-902-45067  
1485 79.5 2.3 481 7 US-11-330-403-13852  
1486 79.5 2.3 495 7 US-11-293-697-4277  
1487 79.5 2.3 504 7 US-11-330-403-1573  
1488 79.5 2.3 504 7 US-11-180-911-2  
1489 79.5 2.3 504 7 US-11-180-911-6  
1490 79.5 2.3 512 6 US-10-449-902-54084  
1491 79.5 2.3 512 6 US-10-449-902-54466

Sequence 18245, A  
Sequence 52923, A  
Sequence 69970, A  
Sequence 73156, A  
Sequence 54720, A  
Sequence 41209, A  
Sequence 45252, A  
Sequence 70345, A  
Sequence 87802, A  
Sequence 873, App  
Sequence 50474, A  
Sequence 70344, A  
Sequence 87801, A  
Sequence 15402, A  
Sequence 238, App  
Sequence 70343, A  
Sequence 87800, A  
Sequence 51182, A  
Sequence 16478, A  
Sequence 17082, A  
Sequence 2, Appli  
Sequence 14115, A  
Sequence 41406, A  
Sequence 41141, A  
Sequence 16140, A  
Sequence 16764, A  
Sequence 6564, App  
Sequence 18, Appl  
Sequence 104646,  
Sequence 115885,  
Sequence 115883,  
Sequence 904, App  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 11, Appl  
Sequence 9410, App  
Sequence 37391, A  
Sequence 35175, A  
Sequence 23990, A  
Sequence 58004, A  
Sequence 14256, A  
Sequence 14255, A  
Sequence 23989, A  
Sequence 58003, A  
Sequence 75, Appl  
Sequence 2866, App  
Sequence 19, Appl  
Sequence 40899, A  
Sequence 49256, A  
Sequence 50065, A  
Sequence 14103, A  
Sequence 48982, A  
Sequence 38367, A  
Sequence 32, Appl  
Sequence 368, App  
Sequence 39826, A  
Sequence 10318, A  
Sequence 79755, A  
Sequence 42963, A  
Sequence 11424, A  
Sequence 2588, App  
Sequence 45067, A  
Sequence 13852, A  
Sequence 4277, App  
Sequence 1573, App  
Sequence 2, Appli  
Sequence 54084, A  
Sequence 54466, A

Search completed: September 5, 2006, 20:24:44  
Job time : 50 secs

1492 79.5 2.3 516 6 US-10-953-349-3991  
1493 79.5 2.3 526 6 US-10-449-902-45168  
1494 79.5 2.3 528 6 US-10-953-349-3990  
1495 79.5 2.3 547 6 US-10-953-349-3989  
1496 79.5 2.3 549 6 US-10-449-902-44979  
1497 79.5 2.3 549 6 US-10-449-902-53417  
1498 79.5 2.3 551 7 US-11-330-403-14884  
1499 79.5 2.3 557 7 US-11-316-521-39  
1500 79.5 2.3 557 7 US-11-330-403-5702  
Sequence 3991, App  
Sequence 45168, A  
Sequence 3990, App  
Sequence 3989, App  
Sequence 44979, A  
Sequence 53417, A  
Sequence 14884, A  
Sequence 39, Appl  
Sequence 5702, App



**THIS PAGE BLANK (USPTO)**























1414 84.5 2.4 600 2 US-10-094-749-2713  
1415 84.5 2.4 658 2 US-09-252-991A-24910  
1416 84.5 2.4 662 2 US-09-902-540-12594  
1417 84.5 2.4 666 2 US-09-248-796A-15507  
1418 84.5 2.4 721 2 US-09-303-518D-514  
1419 84.5 2.4 721 2 US-09-303-518D-520  
1420 84.5 2.4 729 2 US-09-949-016-6544  
1421 84.5 2.4 793 2 US-09-588-256-10  
1422 84.5 2.4 794 2 US-09-949-016-9883  
1423 84.5 2.4 823 2 US-09-107-532A-5667  
1424 84.5 2.4 845 2 US-09-543-661A-4365  
1425 84.5 2.4 886 2 US-09-902-540-14555  
1426 84.5 2.4 919 2 US-09-489-039A-10159  
1427 84.5 2.4 1013 2 US-09-415-522-8  
1428 84.5 2.4 1034 2 US-10-094-749-2631  
1429 84.5 2.4 1157 2 US-09-538-092-1328  
1430 84.5 2.4 1344 2 US-10-104-047-2452  
1431 84.5 2.4 1381 2 US-09-808-701A-25  
1432 84.5 2.4 1498 2 US-09-252-991A-31234  
1433 84.5 2.4 1516 2 US-09-949-016-8209  
1434 84.5 2.4 1565 7 5352450-2  
1435 84.5 2.4 1715 2 US-09-696-115B-17  
1436 84.5 2.4 2042 2 US-09-077-098A-6  
1437 84.5 2.4 2042 2 US-10-192-584-6  
1438 84.5 2.4 2123 2 US-08-968-685A-10  
1439 84.5 2.4 2314 2 US-09-268-347-49  
1440 84.5 2.4 2314 2 US-09-410-551B-72  
1441 84.5 2.4 6396 2 US-09-940-316B-72  
1442 84.5 2.4 45 1 US-08-462-128-39  
1443 84.5 2.4 45 1 US-08-462-180-39  
1444 84.5 2.4 145 2 US-09-252-991A-28281  
1445 84.5 2.4 244 2 US-09-252-991A-18465  
1446 84.5 2.4 283 2 US-09-252-991A-28115  
1447 84.5 2.4 320 2 US-09-134-000C-5021  
1448 84.5 2.4 338 2 US-09-107-532A-5819  
1449 84.5 2.4 342 2 US-09-605-703B-250  
1450 84.5 2.4 361 2 US-09-248-796A-19234  
1451 84.5 2.4 433 2 US-09-046-158A-2  
1452 84.5 2.4 473 2 US-09-538-092-1353  
1453 84.5 2.4 491 2 US-09-712-363-152  
1454 84.5 2.4 502 2 US-09-045-632-24  
1455 84.5 2.4 506 2 US-10-028-180-46  
1456 84.5 2.4 522 2 US-10-172-502-17  
1457 84.5 2.4 583 2 US-09-248-796A-18557  
1458 84.5 2.4 589 2 US-09-489-039A-10810  
1459 84.5 2.4 595 2 US-09-797-039-8  
1460 84.5 2.4 602 2 US-09-045-632-20  
1461 84.5 2.4 616 2 US-09-328-352-5348  
1462 84.5 2.4 630 2 US-09-902-540-11085  
1463 84.5 2.4 646 2 US-09-902-540-12044  
1464 84.5 2.4 648 2 US-09-437-687A-16  
1465 84.5 2.4 648 2 US-10-263-250-16  
1466 84.5 2.4 659 1 US-08-240-049B-16  
1467 84.5 2.4 659 1 US-08-255-18A-20  
1468 84.5 2.4 659 1 US-08-484-054-20  
1469 84.5 2.4 659 1 US-07-876-941A-20  
1470 84.5 2.4 659 2 US-08-477-292-14  
1471 84.5 2.4 659 2 US-07-870-985A-20  
1472 84.5 2.4 681 2 US-09-688-188B-29  
1473 84.5 2.4 681 2 US-09-765-815-2  
1474 84.5 2.4 681 2 US-09-291-417D-29  
1475 84.5 2.4 681 2 US-09-659-737A-10  
1476 84.5 2.4 681 2 US-10-885-921-10  
1477 84.5 2.4 694 2 US-09-949-016-10445  
1478 84.5 2.4 702 2 US-09-045-632-15  
1479 84.5 2.4 714 1 US-08-858-201-2  
1480 84.5 2.4 714 2 US-09-402-214-2  
1481 84.5 2.4 718 2 US-09-949-016-9884  
1482 84.5 2.4 739 2 US-09-035-648-24  
1483 84.5 2.4 739 2 US-09-001-951-24  
1484 84.5 2.4 744 2 US-08-818-829-24  
1485 84.5 2.4 749 2 US-09-902-540-15347  
1486 84.5 2.4 768 2 US-09-328-352-4402

Sequence 2713, Ap  
Sequence 24910, A  
Sequence 12594, A  
Sequence 15507, A  
Sequence 514, App  
Sequence 520, App  
Sequence 6544, Ap  
Sequence 10, App1  
Sequence 9883, Ap  
Sequence 5667, Ap  
Sequence 14555, A  
Sequence 10199, A  
Sequence 2631, Ap  
Sequence 1328, Ap  
Sequence 2452, Ap  
Sequence 25, App1  
Sequence 31234, A  
Sequence 8209, Ap  
Patent No. 5352450  
Sequence 17, App1  
Sequence 6, App1  
Sequence 10, App1  
Sequence 49, App1  
Sequence 72, App1  
Sequence 72, App1  
Sequence 39, App1  
Sequence 39, App1  
Sequence 28281, A  
Sequence 18465, A  
Sequence 28115, A  
Sequence 5021, Ap  
Sequence 5819, Ap  
Sequence 250, App  
Sequence 1934, A  
Sequence 2, App1  
Sequence 153, Ap  
Sequence 15, App  
Sequence 24, App1  
Sequence 46, App1  
Sequence 17, App1  
Sequence 18557, A  
Sequence 10810, A  
Sequence 8, App1  
Sequence 20, App1  
Sequence 5348, Ap  
Sequence 11085, A  
Sequence 12044, A  
Sequence 16, App1  
Sequence 16, App1  
Sequence 16, App1  
Sequence 20, App1  
Sequence 20, App1  
Sequence 20, App1  
Sequence 10, App1  
Sequence 10, App1  
Sequence 10445, A  
Sequence 15, App1  
Sequence 2, App1  
Sequence 2, App1  
Sequence 9884, Ap  
Sequence 24, App1  
Sequence 24, App1  
Sequence 24, App1  
Sequence 15347, A  
Sequence 4402, Ap

1487 84 2.4 776 2 US-09-266-225D-10  
1488 84 2.4 777 2 US-09-949-016-6540  
1489 84 2.4 787 2 US-09-328-352-8055  
1490 84 2.4 793 2 US-09-270-767-42801  
1491 84 2.4 818 2 US-09-045-632-25  
1492 84 2.4 831 2 US-10-360-101-236  
1493 84 2.4 847 2 US-09-373-157-4  
1494 84 2.4 861 2 US-09-045-632-34  
1495 84 2.4 866 2 US-09-949-002-302  
1496 84 2.4 875 2 US-09-949-016-8582  
1497 84 2.4 875 2 US-09-949-002-455  
1498 84 2.4 897 1 US-07-960-389-2  
1499 84 2.4 918 2 US-09-045-632-21  
1500 84 2.4 961 2 US-09-045-632-33

ALIGNMENTS

RESULT 1  
US-09-991-181-179  
Sequence 179, Application US/09991181  
Patent No. 6913919  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Efron, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gember, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC53  
CURRENT APPLICATION NUMBER: US/09/991,181  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28

1 PRIOR APPLICATION NUMBER: 60/087607  
2 PRIOR FILING DATE: 1998-06-02  
3 PRIOR APPLICATION NUMBER: 60/087609  
4 PRIOR FILING DATE: 1998-06-02  
5 PRIOR APPLICATION NUMBER: 60/087759  
6 PRIOR FILING DATE: 1998-06-02  
7 PRIOR APPLICATION NUMBER: 60/087827  
8 PRIOR FILING DATE: 1998-06-03  
9 PRIOR APPLICATION NUMBER: 60/088021  
10 PRIOR FILING DATE: 1998-06-04  
11 PRIOR APPLICATION NUMBER: 60/088025  
12 PRIOR FILING DATE: 1998-06-04  
13 PRIOR APPLICATION NUMBER: 60/088026  
14 PRIOR FILING DATE: 1998-06-04  
15 PRIOR APPLICATION NUMBER: 60/088028  
16 PRIOR FILING DATE: 1998-06-04  
17 PRIOR APPLICATION NUMBER: 60/088029  
18 PRIOR FILING DATE: 1998-06-04  
19 PRIOR APPLICATION NUMBER: 60/088030  
20 PRIOR FILING DATE: 1998-06-04  
21 PRIOR APPLICATION NUMBER: 60/088033  
22 PRIOR FILING DATE: 1998-06-04  
23 PRIOR APPLICATION NUMBER: 60/088326  
24 PRIOR FILING DATE: 1998-06-04  
25 PRIOR APPLICATION NUMBER: 60/088167  
26 PRIOR FILING DATE: 1998-06-05  
27 PRIOR APPLICATION NUMBER: 60/088202  
28 PRIOR FILING DATE: 1998-06-05  
29 PRIOR APPLICATION NUMBER: 60/088212  
30 PRIOR FILING DATE: 1998-06-05  
31 PRIOR APPLICATION NUMBER: 60/088217  
32 PRIOR FILING DATE: 1998-06-05  
33 PRIOR APPLICATION NUMBER: 60/088655  
34 PRIOR FILING DATE: 1998-06-09  
35 PRIOR APPLICATION NUMBER: 60/088734  
36 PRIOR FILING DATE: 1998-06-10  
37 PRIOR APPLICATION NUMBER: 60/088738  
38 PRIOR FILING DATE: 1998-06-10  
39 PRIOR APPLICATION NUMBER: 60/088742  
40 PRIOR FILING DATE: 1998-06-10  
41 PRIOR APPLICATION NUMBER: 60/088810  
42 PRIOR FILING DATE: 1998-06-10  
43 PRIOR APPLICATION NUMBER: 60/088824  
44 PRIOR FILING DATE: 1998-06-10  
45 PRIOR APPLICATION NUMBER: 60/088826  
46 PRIOR FILING DATE: 1998-06-10  
47 PRIOR APPLICATION NUMBER: 60/088858  
48 PRIOR FILING DATE: 1998-06-11  
49 PRIOR APPLICATION NUMBER: 60/088861  
50 PRIOR FILING DATE: 1998-06-11  
51 PRIOR APPLICATION NUMBER: 60/088876  
52 PRIOR FILING DATE: 1998-06-11  
53 PRIOR APPLICATION NUMBER: 60/089105  
54 PRIOR FILING DATE: 1998-06-12  
55 PRIOR APPLICATION NUMBER: 60/089440  
56 PRIOR FILING DATE: 1998-06-16  
57 PRIOR APPLICATION NUMBER: 60/089512  
58 PRIOR FILING DATE: 1998-06-16  
59 PRIOR APPLICATION NUMBER: 60/089514  
60 PRIOR FILING DATE: 1998-06-16  
61 PRIOR APPLICATION NUMBER: 60/089532  
62 PRIOR FILING DATE: 1998-06-17  
63 PRIOR APPLICATION NUMBER: 60/089538  
64 PRIOR FILING DATE: 1998-06-17  
65 PRIOR APPLICATION NUMBER: 60/089598  
66 PRIOR FILING DATE: 1998-06-17  
67 PRIOR APPLICATION NUMBER: 60/089599  
68 PRIOR FILING DATE: 1998-06-17  
69 PRIOR APPLICATION NUMBER: 60/089600  
70 PRIOR FILING DATE: 1998-06-17  
71 PRIOR APPLICATION NUMBER: 60/089653  
72 PRIOR FILING DATE: 1998-06-17  
73 PRIOR APPLICATION NUMBER: 60/089801  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000

PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09  
Query Match 100.0%; Score 3502; DB 2; Length 678;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTTVLTMAKASVIEFVLVTGSHNKETAKKIRKPKFTVQINCVDVAKIIDPEFIV 60  
DB 1 MTTVLTMAKASVIEFVLVTGSHNKETAKKIRKPKFTVQINCVDVAKIIDPEFIV 60  
QY 61 KCPACGDPKHVGTVDVYASVYCGAAVHSGVLDNSGKTLVKKVAGQSGYSYNG 120  
DB 61 KCPACGDPKHVGTVDVYASVYCGAAVHSGVLDNSGKTLVKKVAGQSGYSYNG 120  
QY 121 VQSLSPRWRSEFVILESKPKKGVTPSALTYSKSPAPAGETTKAYQRPPIGTTAQ 180  
DB 121 VQSLSPRWRSEFVILESKPKKGVTPSALTYSKSPAPAGETTKAYQRPPIGTTAQ 180  
QY 181 PVTLMQLLAVTVAATPTTLPRPSPSAATSTIPRQSGVHRSQEMDLMSTATYSSQNR 240  
DB 181 PVTLMQLLAVTVAATPTTLPRPSPSAATSTIPRQSGVHRSQEMDLMSTATYSSQNR 240  
QY 241 PRADGICRQDPSGAFOKPVGADVSLGVPEKEELSTQSLPEVSLGDPNCKIDSLFLDG 300  
DB 241 PRADGICRQDPSGAFOKPVGADVSLGVPEKEELSTQSLPEVSLGDPNCKIDSLFLDG 300  
QY 301 STSICKRRFRIOKOLLADVAQALDIPAGPLMGVVOGDNPAETHNLKTHMTSRDLKTAI 360  
DB 301 STSICKRRFRIOKOLLADVAQALDIPAGPLMGVVOGDNPAETHNLKTHMTSRDLKTAI 360  
QY 361 EKITORGGLSNVGRALISFTVKNFESKANGNSGABNVVVWDGVPDCKVEASRLARES 420  
DB 361 EKITORGGLSNVGRALISFTVKNFESKANGNSGABNVVVWDGVPDCKVEASRLARES 420  
QY 421 GINIFITTEGAENEKQVVEPNPANKAVCTNCFYSLHQSNMGLHKTIOPLYKRVCD 480  
DB 421 GINIFITTEGAENEKQVVEPNPANKAVCTNCFYSLHQSNMGLHKTIOPLYKRVCD 480  
QY 481 TDRLLACSKTCLNSADIGFVIDGSSSVGTGNFETVQFPTNLTKPEISDTPTRIGAVOYT 540  
DB 481 TDRLLACSKTCLNSADIGFVIDGSSSVGTGNFETVQFPTNLTKPEISDTPTRIGAVOYT 540  
QY 541 YEORLEFSGFDKYSKPDILNALKRVYWSGGTSTGAALNFALEQLFKSKENKRLMLLI 600  
DB 541 YEORLEFSGFDKYSKPDILNALKRVYWSGGTSTGAALNFALEQLFKSKENKRLMLLI 600  
QY 601 TDGSSYDVRIPMAAHLKGVITTAIGVMAAOELEVIAITHPADHSFPDEPNLHOY 660  
DB 601 TDGSSYDVRIPMAAHLKGVITTAIGVMAAOELEVIAITHPADHSFPDEPNLHOY 660  
QY 661 VPRIIIONICTEFPNSOPRN 678  
DB 661 VPRIIIONICTEFPNSOPRN 678  
RESULT 2  
US-09-990-444-179  
Sequence 179, Application US/09990444  
Patent No. 6930170  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC19  
CURRENT APPLICATION NUMBER: US/09/990,444  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10



PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540

PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090662  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 2; Length 678;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTMTKASVIEMLVLLVTGHSNKETAKKIKRPFVPOINCDVXAGKIIDPEFIV 60  
1 MRTVLTMTKASVIEMLVLLVTGHSNKETAKKIKRPFVPOINCDVXAGKIIDPEFIV 60  
Db 1 MRTVLTMTKASVIEMLVLLVTGHSNKETAKKIKRPFVPOINCDVXAGKIIDPEFIV 60

QY 61 KCPAGCQDPKHYHYGTDVYASYSVCGAIVHSGVLNDSGKILVRKVAGOSGYKGSYSNG 120  
61 KCPAGCQDPKHYHYGTDVYASYSVCGAIVHSGVLNDSGKILVRKVAGOSGYKGSYSNG 120  
Db 61 KCPAGCQDPKHYHYGTDVYASYSVCGAIVHSGVLNDSGKILVRKVAGOSGYKGSYSNG 120

QY 121 VQSLSPRMRESFIVESKPKKGVTPSALTYSKSPAAOAGETTKAYORPIPGTTAQ 180  
121 VQSLSPRMRESFIVESKPKKGVTPSALTYSKSPAAOAGETTKAYORPIPGTTAQ 180  
Db 121 VQSLSPRMRESFIVESKPKKGVTPSALTYSKSPAAOAGETTKAYORPIPGTTAQ 180

QY 181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSPRPQSVGHSQEMDLSTATYTSSQNR 240  
181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSPRPQSVGHSQEMDLSTATYTSSQNR 240  
Db 181 PVTLMQLLAVTVAVATPTLLPRPSPSAASTTSPRPQSVGHSQEMDLSTATYTSSQNR 240

QY 241 PRADPGIQODPBGGAFOKRVGADVSLGLVPKEELSTOSLEPVSLDDPNCXKIDLSFLDG 300  
241 PRADPGIQODPBGGAFOKRVGADVSLGLVPKEELSTOSLEPVSLDDPNCXKIDLSFLDG 300  
Db 241 PRADPGIQODPBGGAFOKRVGADVSLGLVPKEELSTOSLEPVSLDDPNCXKIDLSFLDG 300

QY 301 STSIGKRRFRIOQLADVAQALDIPAGPLMGVVOGDNPATFMYLKTHTNSRDLTKAI 360  
301 STSIGKRRFRIOQLADVAQALDIPAGPLMGVVOGDNPATFMYLKTHTNSRDLTKAI 360  
Db 301 STSIGKRRFRIOQLADVAQALDIPAGPLMGVVOGDNPATFMYLKTHTNSRDLTKAI 360

QY 361 EKITORGGLSNVGRALISFVTXNFFSKANGNSGAPNVVVVVMDGPTDKVEASRLARBS 420  
361 EKITORGGLSNVGRALISFVTXNFFSKANGNSGAPNVVVVVMDGPTDKVEASRLARBS 420  
Db 361 EKITORGGLSNVGRALISFVTXNFFSKANGNSGAPNVVVVVMDGPTDKVEASRLARBS 420

QY 421 GINIFPTTIEGALENKQYVVEBNFANKAVCRINGSYSLHVQSMFGJLHNTLQPLVRYVCD 480  
421 GINIFPTTIEGALENKQYVVEBNFANKAVCRINGSYSLHVQSMFGJLHNTLQPLVRYVCD 480

Db 421 GINIFFITLEGAEKQVWPPNPNKAVCKTNPFYSLHVQSWGHLKHTIÖPLVKRCD 480  
Qy 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVQFNTNLKEKEISDTPRIGAVOYT 540  
Db 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVQFNTNLKEKEISDTPRIGAVOYT 540  
Qy 541 YEORLEFGFDKYSKPDILNAIKRVGWSGCTSTGAINFALQOLFKSKPKRKLMTLI 600  
Db 541 YEORLEFGFDKYSKPDILNAIKRVGWSGCTSTGAINFALQOLFKSKPKRKLMTLI 600  
Qy 601 TDGRSYDVRIPAMAHKGVTTTAYAGVMAAQEELEVIATHPADHSFPVDEPNLHOY 660  
Db 601 TDGRSYDVRIPAMAHKGVTTTAYAGVMAAQEELEVIATHPADHSFPVDEPNLHOY 660  
Qy 661 VPRITONICTEFNSOPRN 678  
Db 661 VPRITONICTEFNSOPRN 678

RESULT 3  
US-09-997-333-179  
Sequence 179, Application US/09997333  
Patent No. 6853836  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlesen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Grimaldi, U. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: KJavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C27  
CURRENT APPLICATION NUMBER: US/09/997,333  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17

;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089908  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089948  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090246  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090252  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090254  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090355  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090535  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982

;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
Query Match 100.0%; Score 3502; DB 2; Length 678;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRTVVLTMKASVEMFLVLTGSHNKEFKAKIKRPFVPOINCDVAKGIIDDEFIV 60  
DB 1 MRTVVLTMKASVEMFLVLTGSHNKEFKAKIKRPFVPOINCDVAKGIIDDEFIV 60  
QY 61 KCPAGCDDPKYHYGTGVYASVSSVCGAAVHSGVLNDSGKILVRKVAQSGYKGSYNG 120  
DB 61 KCPAGCDDPKYHYGTGVYASVSSVCGAAVHSGVLNDSGKILVRKVAQSGYKGSYNG 120  
QY 121 VQSLSLPRMRESFIVLESKPKKGVTPSALTYSSSSPAQAQETTKAQRPIPGTTAQ 180  
DB 121 VQSLSLPRMRESFIVLESKPKKGVTPSALTYSSSSPAQAQETTKAQRPIPGTTAQ 180  
QY 181 PVTLMQULAVTVAVATPTTLPRPSPAASTTSIPRQSVGHRSQEMDLSTATYSSQNR 240  
DB 181 PVTLMQULAVTVAVATPTTLPRPSPAASTTSIPRQSVGHRSQEMDLSTATYSSQNR 240  
QY 241 PRADPGIORODPSGAAFOKRVGADVSLGLVPKEELSTOSLEPVSLDPPNCKIDLSFLIDG 300  
DB 241 PRADPGIORODPSGAAFOKRVGADVSLGLVPKEELSTOSLEPVSLDPPNCKIDLSFLIDG 300  
QY 301 STSGKRFRRIQQLLADVAQALDIPGAPGLMGVOYGNPRAHFNLTHTNSRDLKTAI 360  
DB 301 STSGKRFRRIQQLLADVAQALDIPGAPGLMGVOYGNPRAHFNLTHTNSRDLKTAI 360  
QY 361 EKITRGGLSNVGRASIFVTKNFSSKANGNRSGAPVWVVMVDGWPJTDKVEASRLARS 420  
DB 361 EKITRGGLSNVGRASIFVTKNFSSKANGNRSGAPVWVVMVDGWPJTDKVEASRLARS 420  
QY 421 GINIFFTIEGAENKQYVVEBNFANKAVCRTNGFYSLHVOSWFLAKTLOPLVRVCD 480  
DB 421 GINIFFTIEGAENKQYVVEBNFANKAVCRTNGFYSLHVOSWFLAKTLOPLVRVCD 480  
QY 481 TDRLACSKTCLNADIGFYIDGSSSVGTGNFRVLQFVNLTKEEISSTDRIGAVQYT 540  
DB 481 TDRLACSKTCLNADIGFYIDGSSSVGTGNFRVLQFVNLTKEEISSTDRIGAVQYT 540  
QY 541 YEORLEFGPDKYSSKEDILNARKVGYMSGSTGTGAINFALBQLFKSKSPNKRKMLILI 600  
DB 541 YEORLEFGPDKYSSKEDILNARKVGYMSGSTGTGAINFALBQLFKSKSPNKRKMLILI 600  
QY 601 TDRGSYDVRIIPMAAHLKGVITYAIGVMAAQEBLEVIATHPARDHSFVDEFDNLHOY 660  
DB 601 TDRGSYDVRIIPMAAHLKGVITYAIGVMAAQEBLEVIATHPARDHSFVDEFDNLHOY 660  
QY 661 VPRIIQNICTEFNSSOPRN 678  
DB 661 VPRIIQNICTEFNSSOPRN 678  
RESULT 4  
US-09-992-598-179  
;; Sequence 179, Application US/09992598  
;; Patent No. 6956108  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Garber, Hanspeter  
;; APPLICANT: Gerlitsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
CURRENT APPLICATION NUMBER: US/09/992,598  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734

PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24

```

; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

```

```

Query Match      100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pired. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRTVVLTMKASVIMFVLVLTGVHSNKETAKKIKRPFTVPOINCVDKAGKIIDPEFIY 60
Db      1 MRTVVLTMKASVIMFVLVLTGVHSNKETAKKIKRPFTVPOINCVDKAGKIIDPEFIY 60

Qy      61 KCPAGCDPKYHYVGTVDVYASYSVCGAAVHSGVLDNSGCKIIVKXVAGSGYKYSYNG 120
Db      61 KCPAGCDPKYHYVGTVDVYASYSVCGAAVHSGVLDNSGCKIIVKXVAGSGYKYSYNG 120

Qy      121 VQSLSLRMRRESFVLSKPKKGTTPSALTYSSSKSPAQAQGTTYAQYRPPITGTTAQ 180
Db      121 VQSLSLRMRRESFVLSKPKKGTTPSALTYSSSKSPAQAQGTTYAQYRPPITGTTAQ 180

Qy      181 PVTLMOLLAVVAATPTTLPRPSPSAASTTISIRPPOSVGHRSQEMDLMSATYTSQNR 240
Db      181 PVTLMOLLAVVAATPTTLPRPSPSAASTTISIRPPOSVGHRSQEMDLMSATYTSQNR 240

Qy      241 PRADPGIORODPSGAAPQPVGADVSLGLVPEKELSTQSLPEVSLGDPNCKIDLSPLIDG 300
Db      241 PRADPGIORODPSGAAPQPVGADVSLGLVPEKELSTQSLPEVSLGDPNCKIDLSPLIDG 300

Qy      301 STSISGKRRFRIOKOLLADVAQALDIPRAGPLMGVVOYGDNPATHFNLKTHNSDLXTAI 360
Db      301 STSISGKRRFRIOKOLLADVAQALDIPRAGPLMGVVOYGDNPATHFNLKTHNSDLXTAI 360

Qy      361 EKITRQGLSNVGAISFTVNGFSSKANGNSGAPNVVVVWVWDMPDVKVEASRLARES 420
Db      361 EKITRQGLSNVGAISFTVNGFSSKANGNSGAPNVVVVWVWDMPDVKVEASRLARES 420

```

```

Qy      421 GINIFPITIEGAENENKQYVEBNFANKVCRITNGFYSLHVQSMFGLHKTLOPLVKRVC 480
Db      421 GINIFPITIEGAENENKQYVEBNFANKVCRITNGFYSLHVQSMFGLHKTLOPLVKRVC 480

Qy      481 TDRLACKTCLNADIGFVIDGSSVGTGNFRVLQFVNLTKEFISDTRIGAVQYT 540
Db      481 TDRLACKTCLNADIGFVIDGSSVGTGNFRVLQFVNLTKEFISDTRIGAVQYT 540

Qy      541 YEQRLFEGFDKYSKSKDILNAIKRVGWSGTSGAINFALBQLFKSKSPNKRKLMILI 600
Db      541 YEQRLFEGFDKYSKSKDILNAIKRVGWSGTSGAINFALBQLFKSKSPNKRKLMILI 600

Qy      601 TDRGRSYDVRIIPMAAHLKGVITYAIGVAAQEELEVIATHPARDHSFFVDEPNLHOY 660
Db      601 TDRGRSYDVRIIPMAAHLKGVITYAIGVAAQEELEVIATHPARDHSFFVDEPNLHOY 660

Qy      661 VPRIIIONICTEFPNSOPRN 678
Db      661 VPRIIIONICTEFPNSOPRN 678

```

```

RESULT 5
US-09-989-735-179
; Sequence 179, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bastein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavian, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989, 735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07

```



;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 2; Length 678;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVVLTKMSVLEMFVLVLVTGHSNKETAKKTKRPFYVPOINCVKAKGIIDPEFIV 60  
DB 1 MRTVVLTKMSVLEMFVLVLVTGHSNKETAKKTKRPFYVPOINCVKAKGIIDPEFIV 60  
QY 61 KCPAGCDDPKHYVGTVDVYASSVSCAAVHSGVLNDSSGKILVRKAVAGSGYKGSYNG 120  
DB 61 KCPAGCDDPKHYVGTVDVYASSVSCAAVHSGVLNDSSGKILVRKAVAGSGYKGSYNG 120  
QY 121 VQSLSPRMBESFVLESKPKKGYTSALTYSKSKPAAQAGTTAYQRPPIGTAAQ 180  
DB 121 VQSLSPRMBESFVLESKPKKGYTSALTYSKSKPAAQAGTTAYQRPPIGTAAQ 180  
QY 181 PVTLMOALATVAATPTLLPRSPSASTTSIPRPSVGHRSQEMLMSTATYSSQNR 240  
DB 181 PVTLMOALATVAATPTLLPRSPSASTTSIPRPSVGHRSQEMLMSTATYSSQNR 240  
QY 241 PRADPGIORODPSGAFOKPVGADVSLGLVPEKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300  
DB 241 PRADPGIORODPSGAFOKPVGADVSLGLVPEKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300  
QY 301 STSGKRRFRIOKOLADVAQALDIGAPLMGVYQGNPAHTFNILKTHNSRDLKTAI 360  
DB 301 STSGKRRFRIOKOLADVAQALDIGAPLMGVYQGNPAHTFNILKTHNSRDLKTAI 360  
QY 361 EKITQRGSLNSVGAISFVTKNFSPSKANGNSGAPNVVVVWDMPDQKVEASRLRES 420  
DB 361 EKITQRGSLNSVGAISFVTKNFSPSKANGNSGAPNVVVVWDMPDQKVEASRLRES 420  
QY 421 GINIFITIGAAENKQYVVEPNFANKAVCRTPGYSLHVSQFGLHKTLOLVKVCVD 480  
DB 421 GINIFITIGAAENKQYVVEPNFANKAVCRTPGYSLHVSQFGLHKTLOLVKVCVD 480  
QY 481 TDRACKSKTCLNSADIGFVIDGSSVGTGNFRYLOFTYNTLTKFEISDPTDRGAVOYT 540  
DB 481 TDRACKSKTCLNSADIGFVIDGSSVGTGNFRYLOFTYNTLTKFEISDPTDRGAVOYT 540  
QY 541 YEORLEGFDPKYSKPDILNAIKVGYWGSSTGGAINFLEQLFKSKRNKAKMILI 600  
DB 541 YEORLEGFDPKYSKPDILNAIKVGYWGSSTGGAINFLEQLFKSKRNKAKMILI 600  
QY 601 TDGRSYDVRIPAMAHLKGVITYAIGVAMAQEELEVIATHPARDHSFVDEFDNLHOY 660  
DB 601 TDGRSYDVRIPAMAHLKGVITYAIGVAMAQEELEVIATHPARDHSFVDEFDNLHOY 660  
QY 661 VPRIIQNICTEFNQOPRN 678  
DB 661 VPRIIQNICTEFNQOPRN 678

RESULT 6  
US-09-989-726-179  
Sequence 179, Application US/09989726

Patent No. 7018811

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Ealon, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerlitsen, Maty E.  
;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P27301C60  
;; CURRENT APPLICATION NUMBER: US/09/989, 726  
;; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/087106  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087609  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088021  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088025  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088030  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09



PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535

PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVVLTKASVTEMFLVLLVTGHSNKEAKKIKRPFVPOINC DVKAGKIIDPEFIV 60  
DB 1 MRTVVLTKASVTEMFLVLLVTGHSNKEAKKIKRPFVPOINC DVKAGKIIDPEFIV 60  
QY 61 KCPAGCDDPKYHYGTDVVAVSYSGCAAVHSGVLNDSGGKILVRKVAGSGYKGSYNG 120  
DB 61 KCPAGCDDPKYHYGTDVVAVSYSGCAAVHSGVLNDSGGKILVRKVAGSGYKGSYNG 120  
QY 121 VQSLSPRMRESFIVLESKRKKGVTYPSALTYSKSPAAQAGETTKAYORPPIPGTTAA 180  
DB 121 VQSLSPRMRESFIVLESKRKKGVTYPSALTYSKSPAAQAGETTKAYORPPIPGTTAA 180  
QY 181 PVTLMOLLAVTVAVAPPTLIPRPSAAGSTTIPRPOSVGHRSQENDLWSTATYTSQNR 240  
DB 181 PVTLMOLLAVTVAVAPPTLIPRPSAAGSTTIPRPOSVGHRSQENDLWSTATYTSQNR 240  
QY 241 PRADPGIORODPSGAFQKRVGADVSLGLVPKRELSTOSLEPVSIGDPNCKIDLSFLIDG 300  
DB 241 PRADPGIORODPSGAFQKRVGADVSLGLVPKRELSTOSLEPVSIGDPNCKIDLSFLIDG 300  
QY 301 STSIGRRRRIQKOLLADVAQALDIPAGPLMGVVOGPNPATHFNLKHTNSRDLKTAI 360  
DB 301 STSIGRRRRIQKOLLADVAQALDIPAGPLMGVVOGPNPATHFNLKHTNSRDLKTAI 360  
QY 361 EKTTOGGLSNVGRASISFTYKFFSKANGNRSGAPVVVVVMDGWTDKVYEASRLARS 420  
DB 361 EKTTOGGLSNVGRASISFTYKFFSKANGNRSGAPVVVVVMDGWTDKVYEASRLARS 420

QY 421 GINIFITIEGAENEQYVVEPNFANKAVCRITNGFSLHVQSWFGHLKTLQPLVKRVC 480  
Db 421 GINIFITIEGAENEQYVVEPNFANKAVCRITNGFSLHVQSWFGHLKTLQPLVKRVC 480  
QY 481 TDRIACSKTCLNSADIGFVIDSSVGTGNFRVLQFVNLTKKEFISDTDRIGAVOYT 540  
Db 481 TDRIACSKTCLNSADIGFVIDSSVGTGNFRVLQFVNLTKKEFISDTDRIGAVOYT 540  
QY 541 YEQRLFEFGPKYSKPTILNAIKRVGWSGTSGAIIINFLBQLFKSKPKNRKXMI 600  
Db 541 YEQRLFEFGPKYSKPTILNAIKRVGWSGTSGAIIINFLBQLFKSKPKNRKXMI 600  
QY 601 TDRSYVDVRIIPMAAHAKGVITVIAIGVMAAOEELVIAITHPARDSFFVDEFDNLHQY 660  
Db 601 TDRSYVDVRIIPMAAHAKGVITVIAIGVMAAOEELVIAITHPARDSFFVDEFDNLHQY 660  
QY 661 VPRIONICTEFPNSOPRN 678  
Db 661 VPRIONICTEFPNSOPRN 678

RESULT 7  
US-09-997-514-179  
Sequence 179, Application US/09997514  
Patent No. 7019116  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C46  
CURRENT APPLICATION NUMBER: US/09/997,514  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089522  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089653  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089801  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089907  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089908  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089947  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/089948  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/089952  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/090246  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090252  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090254  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090349  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090355  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090429  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090431  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090435  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090444  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090445  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090472  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090535  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090540  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090542  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090557  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090676  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090678  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090690  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090694  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090695  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090696  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978

PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTMKASVIMFLVLTGTHSNKETAKKIKRPFYVPOINCDYKAKKIIDPEIV 60  
 DB 1 MRTVLTMKASVIMFLVLTGTHSNKETAKKIKRPFYVPOINCDYKAKKIIDPEIV 60  
 QY 61 KCPAGCDDPKHYVGTVDYVASSVCCAAVHSGVLNDSGKILVRKAGOSGYSGYSG 120  
 DB 61 KCPAGCDDPKHYVGTVDYVASSVCCAAVHSGVLNDSGKILVRKAGOSGYSGYSG 120  
 QY 121 VQSLPRMRRESFVLESKPKKVTYPSALTYSKSPAAQAGETTYAORPPIGTTAQ 180  
 DB 121 VQSLPRMRRESFVLESKPKKVTYPSALTYSKSPAAQAGETTYAORPPIGTTAQ 180  
 QY 181 PVTLMQLLATVAVATPTTLPREPSSAATTSIRPQSVGHRSCQMDLMTATTSSQNR 240  
 DB 181 PVTLMQLLATVAVATPTTLPREPSSAATTSIRPQSVGHRSCQMDLMTATTSSQNR 240  
 QY 241 PRADPGIORODPSGAAPKPGADVSLGLVPKEELSTQSLRPVSLGPNCKIDLSPLIDG 300  
 DB 241 PRADPGIORODPSGAAPKPGADVSLGLVPKEELSTQSLRPVSLGPNCKIDLSPLIDG 300  
 QY 301 STSIGKRRFRIOQLADVAQALDIGPAGPLMGVVOYGDNPAATHFNKTHNSRDLKTAI 360  
 DB 301 STSIGKRRFRIOQLADVAQALDIGPAGPLMGVVOYGDNPAATHFNKTHNSRDLKTAI 360  
 QY 361 EKITQRGSLNVCALISFVTKNPFSSKANGRSGAPNVVWVMDWPTDKVEASRLRES 420  
 DB 361 EKITQRGSLNVCALISFVTKNPFSSKANGRSGAPNVVWVMDWPTDKVEASRLRES 420  
 QY 421 GINIFFTIEGAENEQYVVEPFPANKAVCRTGFFSLHVSFGJHKTLOPLVKRCD 480  
 DB 421 GINIFFTIEGAENEQYVVEPFPANKAVCRTGFFSLHVSFGJHKTLOPLVKRCD 480  
 QY 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRVLOFVTNLTKFEISDTRIGAVQYT 540  
 DB 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRVLOFVTNLTKFEISDTRIGAVQYT 540  
 QY 541 YEQRLERGFDPKYSKPIILNAIKRVGWSGTSFGAINALBOLFKKSKPNKRMILI 600  
 DB 541 YEQRLERGFDPKYSKPIILNAIKRVGWSGTSFGAINALBOLFKKSKPNKRMILI 600  
 QY 601 TDGRSYDVARIPMAAHLKGVITTYAIGVMAAOBELEVIATHPARDHSFVDEEDNLHOY 660  
 DB 601 TDGRSYDVARIPMAAHLKGVITTYAIGVMAAOBELEVIATHPARDHSFVDEEDNLHOY 660  
 QY 661 VPRIIQICTEFPNSQPN 678  
 DB 661 VPRIIQICTEFPNSQPN 678  
 RESULT 8  
 US-09-989-728-179  
 ; Sequence 179, Application us/09989728  
 ; Patent No. 7029873  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gettitsen, Mary E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC72  
CURRENT APPLICATION NUMBER: US/09/989,728  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655

PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24

```

: PRIOR APPLICATION NUMBER: 60/090535
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090540
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090542
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090557
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090676
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090678
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090690
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090694
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090695
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090696
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090862
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/090863
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/091360
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091478
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091544
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091519
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091626
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091978
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091982
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09

```

Query Match 100.0%; Score 3502; DB 3; Length 678;

Best Local Similarity 100.0%; Pred. No. 0; Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRTVVLTKKASVIMFLVLTGYHSNKTAKTKRPFVTPQINCVDYKAGKITIDPEFIV 60
DB 1 MRTVVLTKKASVIMFLVLTGYHSNKTAKTKRPFVTPQINCVDYKAGKITIDPEFIV 60
QY 61 KCPAGCDDPKHYVGTGVYASYSVCGAAVHSGVLNDSGKILVRKXVAGSGYKGSYNSG 120
DB 61 KCPAGCDDPKHYVGTGVYASYSVCGAAVHSGVLNDSGKILVRKXVAGSGYKGSYNSG 120
QY 121 VQSLPRMRESFVLESKEPKKGYTPSALTYSKSKPAAQAGETTYAYORPPIPGTTAAQ 180
DB 121 VQSLPRMRESFVLESKEPKKGYTPSALTYSKSKPAAQAGETTYAYORPPIPGTTAAQ 180
QY 181 PVTLMOLLAATVAAATPTTLPRPSPASATTSIRPQSVGHRSGEMLMSTATYTSQNR 240
DB 181 PVTLMOLLAATVAAATPTTLPRPSPASATTSIRPQSVGHRSGEMLMSTATYTSQNR 240
QY 241 PRADPGIQRDPSGAFOKPYGAVNSIGLVPEKELSQSLPEVSLGDPNCKIDLSFLIDG 300
DB 241 PRADPGIQRDPSGAFOKPYGAVNSIGLVPEKELSQSLPEVSLGDPNCKIDLSFLIDG 300
QY 301 STSIGKRFRIOKQLLDVAQALDIPGAPLMGVVQYGDNPATHFNLKTHNSRDLKTAI 360
DB 301 STSIGKRFRIOKQLLDVAQALDIPGAPLMGVVQYGDNPATHFNLKTHNSRDLKTAI 360
QY 361 EKITQRGLSNVGAISFVTKNFFSKNGNRSGAPNVVVVWVGWPTDXYEASRLARES 420
DB 361 EKITQRGLSNVGAISFVTKNFFSKNGNRSGAPNVVVVWVGWPTDXYEASRLARES 420

```

```

DB 361 EKITQRGLSNVGAISFVTKNFFSKNGNRSGAPNVVVVWVGWPTDXYEASRLARES 420
QY 421 GINIFPTTIGCAANEKQYVEEPFANKAVCRTNGFYSLHVQSMFGHAKTLQPIVKKVCD 480
DB 421 GINIFPTTIGCAANEKQYVEEPFANKAVCRTNGFYSLHVQSMFGHAKTLQPIVKKVCD 480
QY 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRVLOFVTNLTKFEISDTRIGAVOYT 540
DB 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRVLOFVTNLTKFEISDTRIGAVOYT 540
QY 541 YEORLEFGFDKYSKDPILNAIKRVGWSGCTSGAAINFALBOLFCKSKPNKRAKMLILI 600
DB 541 YEORLEFGFDKYSKDPILNAIKRVGWSGCTSGAAINFALBOLFCKSKPNKRAKMLILI 600
QY 601 TDGSRVDDVRIIPMAAHLKGVITTYAIGVAAAOEELVITHPARHDSFVDEFDNLHOY 660
DB 601 TDGSRVDDVRIIPMAAHLKGVITTYAIGVAAAOEELVITHPARHDSFVDEFDNLHOY 660
QY 661 VPRIIQNICTEFNSQPRN 678
DB 661 VPRIIQNICTEFNSQPRN 678

RESULT 9
US-09-997-349-179
: Sequence 179, Application US/09997349
: Patent No. 7034106
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Batton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas P.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PIC37
: CURRENT APPLICATION NUMBER: US/09/997,349
: PRIOR APPLICATION NUMBER: 2001-11-15
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28

```



PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYVLTAKASYIEMLVLTGVSNKETAKIKRPFYQINCDVAKGIIIDPEIV 60  
DB 1 MRYVLTAKASYIEMLVLTGVSNKETAKIKRPFYQINCDVAKGIIIDPEIV 60  
QY 61 KCPAGCOPKHYVTDVYASYSVCGAAVHSGVLDNCGKILVKAQSGSYKSYNG 120  
DB 61 KCPAGCOPKHYVTDVYASYSVCGAAVHSGVLDNCGKILVKAQSGSYKSYNG 120  
QY 121 VQSLPFWRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIGTTAQ 180  
DB 121 VQSLPFWRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIGTTAQ 180  
QY 181 PVTLMQLLAVYVAATPTTLPRPSPASTSIPRPOVGRHSGQMDLWSTATTYSSQNR 240  
DB 181 PVTLMQLLAVYVAATPTTLPRPSPASTSIPRPOVGRHSGQMDLWSTATTYSSQNR 240  
QY 241 PRADPGIOROPSGAFOKPVGADVSLGLVPKEELSTOSLEPVSLGDNCKIDLSFLIDG 300  
DB 241 PRADPGIOROPSGAFOKPVGADVSLGLVPKEELSTOSLEPVSLGDNCKIDLSFLIDG 300  
QY 301 STSIGKRRFRIOKOLLADVAQALDIPAGPLMGVVQYQDNPAHFNLTHTNSRDLKTAI 360  
DB 301 STSIGKRRFRIOKOLLADVAQALDIPAGPLMGVVQYQDNPAHFNLTHTNSRDLKTAI 360  
QY 361 EKITORGGLSNVGRALSVTKNPFSGKANGNSGAPNVVVVVDGCPPTKYVEASRLAES 420  
DB 361 EKITORGGLSNVGRALSVTKNPFSGKANGNSGAPNVVVVVDGCPPTKYVEASRLAES 420  
QY 421 GINIFITIEGAENEKQYVEPNFANKAVCRITNGFSLYHQSMFGHLTKIQLPVKRYCD 480  
DB 421 GINIFITIEGAENEKQYVEPNFANKAVCRITNGFSLYHQSMFGHLTKIQLPVKRYCD 480  
QY 481 TDRIACSKTCLNSADIGFVIDGSSSVGTGNFRYVLFQVYTNLTKEEISDTOTRIQAVOYT 540  
DB 481 TDRIACSKTCLNSADIGFVIDGSSSVGTGNFRYVLFQVYTNLTKEEISDTOTRIQAVOYT 540  
QY 541 YEOHLEFDFKYSKSPDILNAIKRVYSGSTSGAIAINFLBQLFKSKENKXKMLILI 600  
DB 541 YEOHLEFDFKYSKSPDILNAIKRVYSGSTSGAIAINFLBQLFKSKENKXKMLILI 600  
QY 601 TDGSSYDVDRIPAMAHLKGVITYAIGVMAAOELEVITATHPARDSFFVDEFDNLHQY 660  
DB 601 TDGSSYDVDRIPAMAHLKGVITYAIGVMAAOELEVITATHPARDSFFVDEFDNLHQY 660  
QY 661 VPRIIIONICTEFSQPRN 678  
DB 661 VPRIIIONICTEFSQPRN 678

RESULT 10  
US-09-997-653-179  
Sequence 179, Application US/09997653  
Patent No. 7034122  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gettel, Hanspeter

APPLICANT: Gettel, Sherman, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

FILE REFERENCE: P2730P1C38  
CURRENT APPLICATION NUMBER: US/09/997,653  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05

;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09  
;; PRIOR APPLICATION NUMBER: 60/088734  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088742  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088810  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088824  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088858  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089440  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089512  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089532  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089538  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089599  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089600  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089908  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089948  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090246  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090252  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090254  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090355  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472

;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090535  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVVLTMKASVIEMLVLLVTGSHSNKETAKKIKRPKFTVPQINCVDVAKGIIDPEFLV 60  
DB 1 MRTVVLTMKASVIEMLVLLVTGSHSNKETAKKIKRPKFTVPQINCVDVAKGIIDPEFLV 60

QY 61 KCPAGCQDPKHYHYGDDVYASYSVCGAAVHSGVLNDSGKILVRVAQSGYKGSYSNG 120  
DB 61 KCPAGCQDPKHYHYGDDVYASYSVCGAAVHSGVLNDSGKILVRVAQSGYKGSYSNG 120

QY 121 VQSLSPRMRESFIVESKPKKGVTPSALTYSSSKSPAAGETTKAYORPPIPGTTAQ 180  
DB 121 VQSLSPRMRESFIVESKPKKGVTPSALTYSSSKSPAAGETTKAYORPPIPGTTAQ 180

QY 181 PVTLMQLLAVTAATPTTLPRPSPSAASTSIIPRQSVGHSQEMDLNSTATYTSQNR 240  
DB 181 PVTLMQLLAVTAATPTTLPRPSPSAASTSIIPRQSVGHSQEMDLNSTATYTSQNR 240

QY 241 PRADPGIORODPSGAFOKPVGADVSLGVPKRELSLQSLPVSIGDPNCKIDLSPFLIG 300  
DB 241 PRADPGIORODPSGAFOKPVGADVSLGVPKRELSLQSLPVSIGDPNCKIDLSPFLIG 300

QY 301 STSIGRRRRIQKQLADVAQALDIPAGPLMGVVOGNNPATHFNLKTHTSRDLKTAI 360  
DB 301 STSIGRRRRIQKQLADVAQALDIPAGPLMGVVOGNNPATHFNLKTHTSRDLKTAI 360

QY 361 EKITORGSLNNVGRALSFTVKNFESKANGNSGAPNVVVVMDGPTDVKVEASRLARES 420



Db 361 EKTIRGGISNVGRALISFTYKNFESKANGNRSGANNVWWDGPTKVEASRLARES 420  
Qy 421 GINIFITITIEGAENKQYVVEPNFANKAVCTNGFYSILHVSQMGHLKHTLOPLKRCVD 480  
Db 421 GINIFITIEGAENKQYVVEPNFANKAVCTNGFYSILHVSQMGHLKHTLOPLKRCVD 480  
Qy 481 TDRLACSKTCLNSADIGFVNDGSSSVGTGNFRVTLQFVNTLTKEREISDTDRIGAVOYT 540  
Db 481 TDRLACSKTCLNSADIGFVNDGSSSVGTGNFRVTLQFVNTLTKEREISDTDRIGAVOYT 540  
Qy 541 YEORLEFEGFDKXSSKPDILNAIKRQYSGSGTSTAANFALBQLFKSKRNKRLMTLI 600  
Db 541 YEORLEFEGFDKXSSKPDILNAIKRQYSGSGTSTAANFALBQLFKSKRNKRLMTLI 600  
Qy 601 TDGSSYDVRIPAMAAHLKGYTTVAIGVMAAOELEVIAITHPARHSPFVDEPDNLHQY 660  
Db 601 TDGSSYDVRIPAMAAHLKGYTTVAIGVMAAOELEVIAITHPARHSPFVDEPDNLHQY 660  
Qy 661 VPRIIIONICTEFSNQP RN 678  
Db 661 VPRIIIONICTEFSNQP RN 678

## RESULT 11

US-09-989-293A-179

Sequence 179, Application US/09989293A

Patent No. 7034136

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C66  
CURRENT APPLICATION NUMBER: US/09/989, 293A  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089522  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17

;; PRIOR APPLICATION NUMBER: 60/089600  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089908  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089948  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090246  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090252  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090254  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090355  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090535  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633

;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092192  
;; PRIOR FILING DATE: 1998-07-09  
Query Match 100.0%; Score 3502; DB 3; Length 678;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRTVLTMAKASVTEMLVLLVTGSHNKETAKKIKPKFTVPQINDVAKGIIDPEFIY 60  
Db 1 MRTVLTMAKASVTEMLVLLVTGSHNKETAKKIKPKFTVPQINDVAKGIIDPEFIY 60  
QY 61 KCPAGCQDPKHYHYGVGVVYASYSVCGAAGVHSGVLNLSGKILVRVAGSGYKGSYSNG 120  
Db 61 KCPAGCQDPKHYHYGVGVVYASYSVCGAAGVHSGVLNLSGKILVRVAGSGYKGSYSNG 120  
QY 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180  
Db 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180  
QY 181 PVTLMQLLAVTVAVATPTLLPRSPSAASTTSPRQSVGHRSEQMDLWSTATYTSQNR 240  
Db 181 PVTLMQLLAVTVAVATPTLLPRSPSAASTTSPRQSVGHRSEQMDLWSTATYTSQNR 240  
QY 241 PRADPGIQRDPSGAAPQKVGADVSLGLVPKEELSTQSLPEVSLDPPCKIDLSFLIDG 300  
Db 241 PRADPGIQRDPSGAAPQKVGADVSLGLVPKEELSTQSLPEVSLDPPCKIDLSFLIDG 300  
QY 301 STSIGKRRRIQQLADVAQALDIPAGPLMGVVOYGNPAPHNLKHTNSRDLKTAI 360  
Db 301 STSIGKRRRIQQLADVAQALDIPAGPLMGVVOYGNPAPHNLKHTNSRDLKTAI 360  
QY 361 EKITRGGLSNVGRASFPYTKNFFSKANGNRSGAPVVVVMDGPTDVEASRLARES 420  
Db 361 EKITRGGLSNVGRASFPYTKNFFSKANGNRSGAPVVVVMDGPTDVEASRLARES 420  
QY 421 GINIFITTEGAENKQYVVEPNFANKAVCRNGYSYLVHQSDFGLHTLOLVVRVD 480  
Db 421 GINIFITTEGAENKQYVVEPNFANKAVCRNGYSYLVHQSDFGLHTLOLVVRVD 480  
QY 481 TDLRASKTCCLNSADIGFVIDGSSVGTGNFRTVLQFVNLTKEFEISDTRIGAVQYT 540  
Db 481 TDLRASKTCCLNSADIGFVIDGSSVGTGNFRTVLQFVNLTKEFEISDTRIGAVQYT 540  
QY 541 YEQRLEFGDPKYSKPDILINAKRVGVSGSTSGAAINFALEQLFKSKPNKRKLMILI 600  
Db 541 YEQRLEFGDPKYSKPDILINAKRVGVSGSTSGAAINFALEQLFKSKPNKRKLMILI 600  
QY 601 TDRSYDDVRIIPMAHLKGVITYAIGVMAAELEVIATPHARHSPFVDEFDLHOV 660  
Db 601 TDRSYDDVRIIPMAHLKGVITYAIGVMAAELEVIATPHARHSPFVDEFDLHOV 660  
QY 661 VPRIIIONICTEFSOPRN 678  
Db 661 VPRIIIONICTEFSOPRN 678  
RESULT 12  
US-09-907-794A-227  
;; Sequence 227, Application US/09907794A  
;; Patent No. 6635468  
;; GENERAL INFORMATION:  
;; APPLICANT: Genentech, Inc.  
;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT FILING DATE: US/09/907,794A  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 227  
LENGTH: 550  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-907-794A-227

Query March 32.3% Score 1129.5; DB 2; Length 550;  
Best Local Similarity 37.1%; Pred. No. 9.5e-97;  
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

QY 44 INCDVAKGKIIDPERIVKACGDDPKYHVYGVTDVYASYSVCGAAVHSGVLDSGKIL 103  
Db 32 ITCFTRGLDIRKADVLCPGGCPLBERSVYGNIVASVSSICGAAVHSGVSSGCPVR 91  
QY 104 VRKVGOSGYSGYSNGVQSLSPRMRESFVLESKPKKGVTPSALTYSKSPAAQAG 163

Db 92 VYSLGRENYSVDANCIQSOMLSRWSASFVTKGK-----SSTQATQQA- 137  
QY 164 ETRKAYQRPPIPGTTAPVTLMLQLAVTVAATPTLPRPSPAASSTTSIPRQSVGRS 223  
Db 138 -----VSTAH----- 143  
QY 224 QEMDLWSTATYTSQNRPRADPGIQRDPSCGAAFOKPGVADVSLGLVPKELSTQSLBPV 283  
Db 144 -----TPKRLKK-----TPKK----- 156  
QY 284 SLGDPNCKIDSLFLIDSTSIQKRRFRIQQLADVAQALDIPAGFLMGVYQGNPAT 343  
Db 157 -TGKDKADIAFLIDSFNIGORFNLQKPFVKALMLGIGEGHVGIVQASEHPKI 215  
QY 344 HFNKHTNSRDKTAEIKTORGGLSNVGRALISFVTKFNFSKANGRSKGNVGVVMD 403  
Db 216 EFLYAKNTSAKDVPFAIKVGFPGNSNTGALKHTQKFFTYDAGVRKGIKPVVVVFID 275  
QY 404 GMPYDKVEASRLARESGINIFLTTEGAAENKQYVVEBNFANKAVCRTNGFYSLHVQS 463  
Db 276 GMPSDIEEAGIYARFVGAVVFIYSVAKPIBELGMVQDVTVPYDKAVCRNNGFESYHMPN 335  
QY 464 WFGHLKTLQPLVYKVCOTDRKLACSKTCLNSADIGFVIDSSSVGTGFRVLYQVYMLTK 523  
Db 336 WFGTKYKPLVYKLCHEQMCMCSKTCYNVNIATFLIDGSSSVGDSNFRMLLEFVSNIAK 395  
QY 524 EPEISDPTRIQAVQYVEORLEFGFDKYSKXPDILNARIKVGWSGSTGGAINFAL 583  
Db 396 TFEISDIGAKIAAVQFYDRTFESFTDYSTKENVLVINIRYMSGTATGDAISTTVR 455  
QY 584 QLFK--KSKPNKRLMLITDGRSYDDVRIPAMAHLKGIYTAIGVMAAOBELVIAT 641  
Db 456 NVFGPIRESNK-NFLVITVDGOSYDDVQPAAAAHADAGITISVGAAMPPLDDLKOMAS 514  
QY 642 HPARDSFVDEEDNLHQVPRITIQNICTEF 672  
Db 515 KPKESHAFFTRFETGLEPIVSDVIRGICRDF 545

RESULT 13  
US-09-905-125A-227  
Sequence 227, Application US/09905125A  
Patent No. 6664376  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14



```
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 227
;; LENGTH: 550
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-906-775A-227
```

```
Query Match 32.3% Score 1129.5; DB 2; Length 550;
Best Local Similarity 37.1%; Pred. No. 9.5e-97;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;
```

```
QY 44 INCDVAKGIIDPEFIVKPCAGCDPKYHVYGTVDVYSSVCGAAVHSGVLNDSGKIL 103
Db 32 ITCTRGIDIRKADVLCPGGCPLLEBSYGNIVASVSSICGAHVHGVISNSGGVVR 91
QY 104 VRKAGSGGYKGSNGVQSLSPWRMSFVLESKPKGVYTSALTYSKSPAAQAG 163
Db 92 VYSLPGRNYSVANGVQSQMLSRMSASFVTVKTK-----SSTQATQGA- 137
QY 164 ETTAVYORPPIPGTTAQVTLMLLAIVVAATPTTLPRPSPASASTSIRPQSVGRS 223
Db 138 -----VSTAHF----- 143
QY 224 QEMDLWSTATYVTSQNRPRADPGIORDPGSAFAQKPVGADVSLGLVPEKELSTQSLPEV 283
Db 144 -----PTGKRLKK-----TPKK----- 156
QY 284 SLGDPNCKIDSLFDGSTIGKRRFRIQKQLADVAQALDIGAPGLMGVGYGDNPAT 343
Db 157 -TGKDCADIAFLIDGSFNIGORFNIQKNFVKVLMIGIGTEGPHVGLVQASEHPKI 215
QY 344 HFNKTHNSRDLTAITEKIQRGSLNVGRALISFVTKNFSKANGRSQAPNVVVMVD 403
Db 216 EFYIKNFTSAQDVLPALKEVGFGRGNSNTGKALXHTAQKFTVDAGVRKGIPIKVVVFI 275
QY 404 GMPYDVEASRLARESGINIFITIEGAANEKQYVVEPFAKAVACRTGTFYSLHVS 463
Db 276 GWPEDDIEBAGIVAREGVNVFIVSAKPIPEELGMQDVTFFVDAKACRRNNGFSYMPN 335
QY 464 WFGIHLKLOLVKVCYCTDLRACSKTCLNSADIPFVIDGSSSVGTGNFRVYLOFVNLTK 523
Db 336 WFGITKLVKLVQKLCHEQWMCCKTCNSVNI AFLIDGSSSVDSNFRMLLEFVSNIAK 395
QY 524 EPEISDUTRIGAVQYTEORLEFGPKYSKPIULNAIKRVGWSGTSGAALNPALE 583
Db 396 TFEISDYGAKIAAQQFYTDQRTESFYDYSTEKENVLAVIRIKRWSGGTADGDISFTVR 455
QY 584 QLFK-KSKPNKRLMLITDGRSYDVVRIAPMAAHLKGVITVAIGVMAAQEELVIAT 641
Db 456 NVFPIRESPPK-NFLVIVTDGQSYDDVQGPAAAHAGITFISVGVAMAPLDDLKQMAS 514
QY 642 HPAADHSFVDEPNLQVYPRITQNTCTER 672
Db 515 KPKEASHAFTRFGLPIVSDVIRGICRDP 545
```

RESULT 15  
US-09-906-700-227

```
;; Sequence 227, Application US/09906700
;; Patent No. 6723535
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gertschen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/906,700
;; CURRENT FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 227
;; LENGTH: 550
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-906-700-227
```



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2006, 20:00:53 ; Search time 306 Seconds  
(without alignments)  
2049.544 Million cell updates/sec

Title: US-10-063-538-34

Perfect score: 3502  
Sequence: 1 MRLVLTMKASVIEFLVL.....QYVRIQICTEFNQPRN 678

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Uniprot\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3502	100.0	678	Q6UX17_HUMAN	Q6UX17 homo sapien
2	3484.5	99.5	693	Q9UDN0_HUMAN	Q9UDN0 homo sapien
3	3344	95.5	656	Q96DT1_HUMAN	Q96DT1 homo sapien
4	2826	80.7	650	Q3T247_MOUSE	Q3T247 mus musculus
5	2823	80.6	650	Q8VHT5_MOUSE	Q8VHT5 mus musculus
6	2818	80.5	652	Q95L12_BOVIN	Q95L12 bos taurus
7	2801	80.0	650	Q8K047_MOUSE	Q8K047 mus musculus
8	2796	79.8	650	Q9CY21_MOUSE	Q9CY21 mus musculus
9	2682	76.6	628	Q8BQ41_MOUSE	Q8BQ41 mus musculus
10	2311.5	66.0	748	Q5NTW9_CHICK	Q5NTW9 gallus galli
11	1929	55.1	680	Q4RP27_TETNG	Q4RP27 tetractadon n
12	1187.5	33.9	553	Q8AW56_BRARE	Q8AW56 brachydanio n
13	1139	32.5	547	COCH_HUMAN	COCH4163 gallus galli
14	1129.5	32.3	550	COCH_HUMAN	COCH405 homo sapien
15	1123.5	32.1	550	Q50EA4_BOVIN	Q50EA4 bos taurus
16	1115	31.8	552	Q3U021_MOUSE	Q3U021 mus musculus
17	1113	31.8	552	COCH_MOUSE	Q62507 mus musculus
18	1113	31.8	552	Q3TAF5_MOUSE	Q3TAF5 mus musculus
19	1017.5	29.1	494	Q96I06_HUMAN	Q96I06 homo sapien
20	1008.5	28.8	586	Q4T252_TETNG	Q4T252 tetractadon n
21	848	24.2	203	Q6P7T3_HUMAN	Q6P7T3 homo sapien
22	834.5	23.8	401	Q6ZP09_HUMAN	Q6ZP09 homo sapien
23	554	15.8	3124	COCA1_CHICK	P13944 gallus galli
24	552	15.8	3119	COCA1_MOUSE	Q60847 mus musculus
25	543.5	15.5	3063	COCA1_HUMAN	Q99715 homo sapien
26	542.5	15.5	2884	Q5VYK2_HUMAN	Q5VYK2 homo sapien
27	542.5	15.5	3063	Q5VYK1_HUMAN	Q5VYK1 homo sapien
28	512	14.6	490	Q7SVT5_XENLA	Q7SVT5 xenopus lae
29	505	14.4	490	Q5BK6_XENR	Q5BK6 xenopus tro
30	504.5	14.4	3137	COCA3_CHICK	P15969 gallus galli
31	501.5	14.3	496	MATN1_HUMAN	P21941 homo sapien

32	501.5	14.3	496	Q5TBB9_HUMAN	Q5TBB9 homo sapien
33	494.5	14.1	498	Q5X124_RAT	Q5X124 rattus norv
34	493	14.0	500	Q80V55_MOUSE	Q80V55 mus musculus
35	490	14.0	493	MATN1_CHICK	P05099 gallus galli
36	489	14.0	500	MATN1_MOUSE	P51942 mus musculus
37	488.5	13.9	1259	Q4RP12_TETNG	Q4RP12 tetractadon n
38	485	13.8	507	Q7ZVP3_BRARE	Q7ZVP3 brachydanio
39	478.5	13.7	644	Q5NJU1_BRARE	Q5NJU1 brachydanio
40	471.5	13.5	2588	Q53OP4_HUMAN	Q53OP4 homo sapien
41	471.5	13.5	3176	CO6A3_HUMAN	P12111 homo sapien
42	466	13.3	3169	Q4KRT6_CANFA	Q4KRT6 canis fami
43	464	13.2	1453	Q4RNL1_TETNG	Q4RNL1 tetractadon n
44	463	13.2	1182	Q8CEK9_MOUSE	Q8CEK9 mus musculus
45	459	13.1	685	Q5NJU2_BRARE	Q5NJU2 brachydanio
46	446.5	12.7	647	Q4S2X7_TETNG	Q4S2X7 tetractadon n
47	439.5	12.5	726	Q5NJI4_BRARE	Q5NJI4 brachydanio
48	435.5	12.4	1703	Q92019_MOUSE	Q92019 mus musculus
49	432.5	12.4	1636	Q4TBC0_TETNG	Q4TBC0 tetractadon n
50	430.5	12.3	622	MATN4_HUMAN	Q95460 homo sapien
51	416.5	11.9	1222	Q63HQ4_HUMAN	Q63HQ4 homo sapien
52	415.5	11.9	1723	Q4SD22_TETNG	Q4SD22 tetractadon n
53	412.5	11.8	624	MATN4_MOUSE	Q89029 mus musculus
54	403.5	11.5	821	Q6PYX2_BRARE	Q6PYX2 brachydanio
55	400.5	11.4	2225	Q4SKX3_TETNG	Q4SKX3 tetractadon n
56	385.5	11.0	4421	Q4RK60_TETNG	Q4RK60 tetractadon n
57	380.5	10.9	840	Q32NR2_XENLA	Q32NR2 xenopus lae
58	378	10.8	790	Q6DCQ6_XENLA	Q6DCQ6 xenopus lae
59	378	10.8	2657	Q88493_MOUSE	Q88493 mus musculus
60	369.5	10.6	839	Q6P3N7_XENR	Q6P3N7 xenopus tro
61	357.5	10.2	956	MATN2_HUMAN	Q00339 homo sapien
62	352.5	10.1	349	Q4SB12_TETNG	Q4SB12 tetractadon n
63	350.5	10.0	955	Q5R9N1_PONPY	Q5R9N1 pongo pygma
64	350.5	10.0	1797	COEAL1_MOUSE	Q80X19 mus musculus
65	343.5	9.8	717	Q4RG72_TETNG	Q4RG72 tetractadon n
66	342	9.8	944	Q5NUJ5_BRARE	Q5NUJ5 brachydanio
67	341	9.7	534	Q4G0W3_HUMAN	Q4G0W3 homo sapien
68	341	9.7	1796	COEAL1_HUMAN	Q05707 homo sapien
69	339.5	9.7	956	Q99K64_MOUSE	Q99K64 mus musculus
70	338.5	9.7	919	Q75RS2_LYMET	Q75RS2 lymphoc ste
71	337.5	9.6	928	Q3TQ80_MOUSE	Q3TQ80 mus musculus
72	337.5	9.6	937	Q563V0_MOUSE	Q563V0 mus musculus
73	337.5	9.6	956	MATN2_MOUSE	Q08746 mus musculus
74	337.5	9.6	956	Q8R542_MOUSE	Q8R542 mus musculus
75	334	9.5	721	Q8CE01_MOUSE	Q8CE01 mus musculus
76	333	9.5	791	Q70U27_MOUSE	Q70U27 mus musculus
77	333	9.5	791	Q3UM88_MOUSE	Q3UM88 mus musculus
78	332.5	9.5	725	Q6ZS39_HUMAN	Q6ZS39 mus musculus
79	331	9.5	1888	COEAL1_CHICK	Q6B839 homo sapien
80	329.5	9.4	2944	CO7A1_HUMAN	P32018 gallus galli
81	326.5	9.3	950	Q4RK59_TETNG	Q4RK59 tetractadon n
82	326	9.3	1253	Q97566_CANFA	Q97566 canis fami
83	326	9.3	2936	Q7YRK8_CANFA	Q7YRK8 canis fami
84	325.5	9.3	725	Q6ZNU7_HUMAN	Q6ZNU7 homo sapien
85	325.5	9.3	755	Q5GFL6_HUMAN	Q5GFL6 homo sapien
86	325.5	9.3	755	Q70U28_HUMAN	Q70U28 homo sapien
87	324	9.3	2944	Q63870_MOUSE	Q63870 mus musculus
88	323	9.2	517	Q43853_HUMAN	Q43853 homo sapien
89	314.5	9.0	688	Q4TCK3_TETNG	Q4TCK3 tetractadon n
90	313	8.9	453	Q8TSC2_MYTGA	Q8TSC2 mytilus gal
91	310.5	8.9	565	Q18048_CABEL	Q18048 caenorhabdi
92	307	8.8	444	Q8TSC3_MYTED	Q8TSC3 mytilus edu
93	305	8.7	428	Q5NUJ0_BRARE	Q5NUJ0 brachydanio
94	300	8.6	441	Q8TEU5_MYRED	Q8TEU5 mytilus edu
95	299.5	8.6	1450	Q4RP14_TETNG	Q4RP14 tetractadon n
96	298	8.5	537	Q96A40_HUMAN	Q96A40 homo sapien
97	296	8.5	261	Q5CZ06_BRARE	Q5CZ06 brachydanio
98	295	8.4	1557	Q4SH63_TETNG	Q4SH63 tetractadon n
99	291.5	8.3	2101	Q61XK2_CABBR	Q61XK2 caenorhabdi
100	290.5	8.3	954	Q8XWV8_HUMAN	Q8XWV8 homo sapien
101	290.5	8.3	957	Q9H0V3_HUMAN	Q9H0V3 homo sapien
102	290.5	8.3	957	Q96P44_HUMAN	Q96P44 homo sapien
103	289.5	8.3	1626	Q8NFW1_HUMAN	Q8NFW1 homo sapien
104	287	8.2	1380	Q4S053_TETNG	Q4S053 tetractadon n





251	232	6.6	421	2	Q9EPPE_9HYST	Q9EPPE_clethronomys ma	324	221	6.3	407	2	Q28357_DOBMO	Q28357_dobsonia mo
252	231.5	6.6	390	2	Q5GN58_9HYST	Q5GN58 tritomyia pa	325	221	6.3	920	2	Q28984_PIG	Q28984 sus scrofa
253	231.5	6.6	402	2	Q9TSP0_PROPH	Q9TSP0 phococnoid	326	220.5	6.3	357	2	Q60YE1_CABER	Q60YE1 caenorhabdi
254	231.5	6.6	409	2	Q77671_ECHTE	Q77671 echinops te	327	220.5	6.3	385	2	Q5GN56_9HYST	Q5GN56 tritomyia yo
255	231	6.6	385	2	Q91YE7_9RODE	Q91YE7 macrocrasom	328	220.5	6.3	385	2	Q91YH3_CRIGA	Q91YH3 cricetomyia
256	231	6.6	385	2	Q91YH2_CLEGL	Q91YH2 clethrionom	329	220.5	6.3	395	2	Q77673_CHAVI	Q77673 chaetophnac
257	231	6.6	387	2	Q8HXU1_PRIMA	Q8HXU1 pitodontes	330	220.5	6.3	403	2	Q9MZE8_DELE	Q9MZE8 delphinapte
258	231	6.6	410	2	Q9Z114_ALLACTA	Q9Z114 allactaga e	331	220.5	6.3	411	2	Q9EPD4_9HYST	Q9EPD4 petromus ty
259	231	6.6	421	2	Q9EQS2_AARBE	Q9EQS2 abrococna be	332	220.5	6.3	415	2	Q2MDK4_9HYST	Q2MDK4 pyrorictes
260	231	6.6	1152	1	ITAM_HUMAN	P11215 homo sapien	333	220	6.3	385	2	Q91YAS_TATGH	Q91YAS latera kemp
261	231	6.6	1152	2	Q4VAKO_HUMAN	Q4VAKO homo sapien	334	220	6.3	385	2	Q91YG4_9RODE	Q91YG4 gerbillus h
262	231	6.6	1152	2	Q4VAK1_HUMAN	Q4VAK1 homo sapien	335	220	6.3	385	2	Q91YH0_9RODE	Q91YH0 calomyscus
263	231	6.6	1152	2	Q4VAK2_HUMAN	Q4VAK2 homo sapien	336	220	6.3	409	2	Q9TSP7_GALGR	Q9TSP7 galago cras
264	230.5	6.6	413	2	Q2MDK5_9EUTH	Q2MDK5 limnogale m	337	219.5	6.3	391	2	Q5GN67_9HYST	Q5GN67 dactylomyia
265	229.5	6.6	383	2	Q5GN59_9HYST	Q5GN59 thricomyia h	338	219.5	6.3	408	2	Q7YRM5_9EUTH	Q7YRM5 elephanthinu
266	229.5	6.6	402	2	Q8WN27_NYCAL	Q8WN27 nyctilimene a	339	219.5	6.3	421	2	Q9JXK18_MASWZ	Q9JXK18 massoutiera
267	229.5	6.6	414	2	Q2MDL1_GALLEE	Q2MDL1 gallidia ele	340	219.5	6.3	1162	1	ITAD_HUMAN	Q13349 homo sapien
268	229	6.5	365	2	Q64216_9RODE	Q64216 spalax zemm	341	219.5	6.3	1177	2	Q59H14_HUMAN	Q59H14 homo sapien
269	229	6.5	385	2	Q91YGS_9RODE	Q91YGS dictyostomyx	342	219	6.3	381	2	Q5G5W2_CRATH	Q5G5W2 craseonycte
270	229	6.5	421	2	Q9EPPE_9HYST	Q9EPPE cryptomyia h	343	218.5	6.2	393	2	Q91YG3_JACJA	Q91YG3 jaculus jac
271	229	6.5	572	2	Q21540_CABEL	Q21540 caenorhabdi	344	218.5	6.2	393	2	Q9GL87_MESPE	Q9GL87 mesopodion
272	229	6.5	967	2	Q3UIW4_MOUSE	Q3UIW4 mus musculu	345	218	6.2	396	2	Q6JC71_9EUTH	Q6JC71 solenodon p
273	229	6.5	1064	2	Q3TBT0_MOUSE	Q3TBT0 mus musculu	346	218	6.2	398	2	Q9TSU5_PELCA	Q9TSU5 felis silve
274	229	6.5	1153	1	ITAM_MOUSE	P05555 mus musculu	347	218	6.2	403	2	Q8WN32_NOCAL	Q8WN32 noctilio al
275	229	6.5	1153	2	Q3TDB6_MOUSE	Q3TDB6 mus musculu	348	218	6.2	414	2	Q2MDL2_FOSFO	Q2MDL2 fossa fossa
276	229	6.5	1153	2	Q3U415_MOUSE	Q3U415 mus musculu	349	217.5	6.2	365	2	Q8WNM57_ROUM	Q8WNM57 rousetus a
277	229	6.5	1166	2	Q3U3F0_MOUSE	Q3U3F0 mus musculu	350	216	6.2	385	2	Q91YCA_9RODE	Q91YCA nesomyia ruf
278	229	6.5	1232	2	Q3UIU4_MOUSE	Q3UIU4 mus musculu	351	215.5	6.2	383	2	Q5GN61_9HYST	Q5GN61 proechinys
279	228.5	6.5	391	2	Q5GN69_MESHI	Q5GN69 mesomys his	352	215.5	6.2	410	2	Q8M157_PLENU	Q8M157 pleectus au
280	228.5	6.5	414	2	Q2MDK6_CRYPE	Q2MDK6 cryptoproct	353	215.5	6.2	421	2	Q2MDK1_VIVIN	Q2MDK1 viverricula
281	228.5	6.5	421	2	Q9UK21_CHILA	Q9UK21 chindhilla	354	214.5	6.1	2401	2	Q7RF52_PLAYO	Q7RF52 plasmiodum
282	228.5	6.5	789	2	Q9BKQ4_CABEL	Q9BKQ4 caenorhabdi	355	214	6.1	399	2	Q5G5W4_FURO	Q5G5W4 furipterus
283	228	6.5	417	2	Q9ZOR2_9HYST	Q9ZOR2 sphigyrus	356	214	6.1	409	2	Q5SKU5_CHODI	Q5SKU5 choloepus d
284	228	6.5	410	2	Q9Z0Q3_MARMO	Q9Z0Q3 marmota mon	357	214	6.1	1169	2	Q3UIP9_MOUSE	Q3UIP9 mus musculu
285	228	6.5	1028	1	CO6A1_HUMAN	P12109 homo sapien	358	213.5	6.1	411	2	Q9JXK17_PEDCA	Q9JXK17 pedetes cap
286	228	6.5	1163	1	ITAX_HUMAN	P72645 homo sapien	359	213.5	6.1	414	2	Q28904_PIG	Q28904 sus scrofa
287	228	6.5	411	2	Q9GL88_HINIGE	P20702 homo sapien	360	213.5	6.1	1286	2	Q9TXR6_CABEL	Q9TXR6 caenorhabdi
288	227.5	6.5	445	2	Q9BSA8_HUMAN	Q9BSA8 hnia geoffr	361	213	6.1	2255	2	Q4SD21_TETNG	Q4SD21 tetraodon n
289	227.5	6.5	421	2	Q9EPN7_HELAR	Q9EPN7 heliohaplu	362	212.5	6.1	390	2	Q7YR18_PTEPA	Q7YR18 pteronodon n
290	227	6.5	421	2	Q9JKO2_9HYST	Q9JKO2 octodon lun	363	212.5	6.1	406	2	Q8WN26_DESKO	Q8WN26 desmodus ro
291	227	6.5	413	2	Q2MDK2_SURSU	Q2MDK2 suricata su	364	212.5	6.1	1161	1	ITAD_RAT	Q9JXK17 rat
292	226.5	6.5	413	2	Q2MDK2_SURSU	Q2MDK2 suricata su	365	212	6.1	358	2	Q9TV39_TUPEL	Q9TV39 tupia glis
293	226.5	6.5	427	2	Q28349_CYNVA	Q28349 cynocephalu	366	212	6.1	365	2	Q9XSA4_LAMGL	Q9XSA4 lama glama
294	226.5	6.5	439	2	Q8TBNZ_HUMAN	Q8TBNZ homo sapien	367	212	6.1	410	2	Q19029_9EUTH	Q19029 mans sp. v
295	226.5	6.5	1025	1	CO6A1_MOUSE	Q04857 mus musculu	368	212	6.1	410	2	Q8M160_TADIN	Q8M160 tadrida in
296	225.5	6.4	408	2	Q5GN57_9HYST	Q5GN57 tritomyia se	369	212	6.1	423	2	Q8M164_BRATR	Q8M164 bradypus tr
297	225.5	6.4	414	2	Q7YRP9_NYCCO	Q7YRP9 nycticebus	370	212	6.1	1169	1	ITAX_MOUSE	Q9JXK14 mus musculu
298	225.5	6.4	387	2	Q2MDJ3_9CARN	Q2MDJ3 eulaptes go	371	212	6.1	200	2	Q3TDI3_MOUSE	Q3TDI3 mus musculu
299	225	6.4	391	2	Q5GN55_9HYST	Q5GN55 eurzygomat	372	211.5	6.0	323	2	Q7YXQ9_NORTY	Q7YXQ9 notoryctes
300	225	6.4	399	2	Q2MDK6_LEPED	Q2MDK6 lepilemur e	373	211.5	6.0	410	2	Q8M153_EPTNI	Q8M153 eptesicus n
301	225	6.4	417	2	Q9Z0MS_THRSW	Q9Z0MS thryonomys	374	211.5	6.0	410	2	Q8M158_9CHIR	Q8M158 barbastella
302	225	6.4	421	2	Q2MDL7_CROCR	Q2MDL7 crocuta cro	375	211.5	6.0	639	1	COCA1_EABIT	Q28992 cyclopterus
303	224.5	6.4	1060	2	Q4SQ43_TETNG	Q4SQ43 tetraodon n	376	211.5	6.0	410	2	Q8M159_9CHIR	Q8M159 miniopterus
304	224.5	6.4	387	2	Q95KS9_MYRIR	Q95KS9 myrmecophag	377	211	6.0	1188	2	Q6KAS4_MOUSE	Q6KAS4 mus musculu
305	224	6.4	412	2	Q8HXM8_TALEU	Q8HXM8 talpa europ	378	210.5	6.0	385	2	Q91YV4_9RODE	Q91YV4 tachyorycte
306	224	6.4	368	2	Q28364_EQUAS	Q28364 equus asinu	379	210.5	6.0	389	2	Q8WN35_9CHIR	Q8WN35 nyctereis gr
307	223.5	6.4	411	2	Q9EPF7_ATHMA	Q9EPF7 atherurus m	380	210.5	6.0	410	2	Q8M150_9CHIR	Q8M150 murina usu
308	223	6.4	383	2	Q9MZE6_TIPCA	Q9MZE6 ziphius cav	381	210.5	6.0	862	2	Q615W4_CABER	Q615W4 caenorhabdi
309	223	6.4	383	2	Q5GN54_9HYST	Q5GN54 proechinys	382	210.5	6.0	2098	2	Q25757_PLAFA	Q25757 plasmiodum
310	222.5	6.4	383	2	Q5GN68_9HYST	Q5GN68 thricomyia lat	383	210	6.0	397	2	Q5GN64_9HYST	Q5GN64 kanabatomus
311	222.5	6.4	407	2	Q7YRM3_MACPR	Q7YRM3 macroscelid	384	210	6.0	421	2	Q7YR17_MYSTU	Q7YR17 mystecata t
312	222.5	6.4	408	2	Q7YRM6_PETTE	Q7YRM6 petrodromus	385	210	6.0	421	2	Q9JXK18_CTEVA	Q9JXK18 ctenodactyl
313	222.5	6.4	1268	2	Q616M0_CABER	Q616M0 caenorhabdi	386	209.5	6.0	467	2	Q4RBL7_TETNG	Q4RBL7 tetraodon n
314	222.5	6.4	350	2	Q5GN65_9HYST	Q5GN65 isotheria si	387	209.5	6.0	1022	1	CO6A2_CHICK	Q91368 gallus galli
315	222	6.3	365	2	Q8MKN2_9ROUM	Q8MKN2 rousetus a	388	209.5	6.0	385	2	Q920U8_ACCOA	Q920U8 acromys cahi
316	222	6.3	385	2	Q8HXU7_DASKA	Q8HXU7 dasypus kap	389	208.5	6.0	410	2	Q8M156_9CHIR	Q8M156 scotophilus
317	222	6.3	410	2	Q8WN30_9CHIR	Q8WN30 thimolophus	390	208	5.9	2957	2	Q4REB8_TETNG	Q4REB8 tetraodon n
318	222	6.3	385	2	Q9T140_HIPCO	Q9T140 hipposidero	391	207.5	5.9	410	2	Q8M152_VESSU	Q8M152 vesperfilio
319	222	6.3	1125	2	Q2UYO9_HUMAN	Q2UYO9 homo sapien	392	207.5	5.9	1170	1	ITALL_HUMAN	Q20701 homo sapien
320	222	6.3	385	2	Q91YR8_MESAV	Q91YR8 mesocricetu	393	207.5	5.9	1170	2	Q5NKT6_PANTR	Q5NKT6 pan troglod
321	221.5	6.3	405	2	Q7YRM8_9EUTH	Q7YRM8 elephanthinu	394	207	5.9	410	2	Q9T143_MOVE	Q9T143 myotis vell
322	221.5	6.3	385	2	Q91YCS_NEOFU	Q91YCS neotoma fus	395	207	5.9	960	2	Q4RSP3_TETNG	Q4RSP3 tetraodon n
323	221	6.3	385	2			396	207	5.9				

397	206.5	5.9	146	2	OSTF09_HUMAN	O5tcf9	homo sapien	470	188.5	5.4	1171	2	042094_CHICK	042094	gallus gall
398	206.5	5.9	391	2	08WN28_NYCTH	08wn28	mycteris th	471	188.5	5.4	1620	2	08IK83_PLAF7	08IK83	plasmodium
399	206	5.9	410	2	08M151_MYOVA	08m151	myotis yarb	472	187.5	5.4	1170	1	ITAI2_BOVIN	ITAI2	bovin
400	205.5	5.9	382	2	091VG7_9RODE	091vg7	deomys ferr	473	187.5	5.4	1188	1	ITAI1_MOUSE	ITAI1	mouse
401	205	5.9	979	2	08N471_HUMAN	08n471	homo sapien	474	187	5.3	146	2	04KTM5_CEREI	04KTM5	cervus elap
402	205	5.9	1029	1	CO6A2_MOUSE	002782	homo sapien	475	187	5.3	1197	2	04UB99_THEAN	04UB99	thelateria a
403	205	5.9	1034	2	08K229_MOUSE	08k229	mus musculus	476	186	5.3	1070	2	04N1E8_THEPA	04N1E8	thelateria p
404	204.5	5.8	831	2	04Y774_PLACH	04y774	plasmodium	477	185	5.3	269	2	08OWE9_RAT	08OWE9	rattus norv
405	204	5.8	343	2	08WN34_ANTPA	08wn34	antrozous p	478	184.5	5.3	322	2	07YXO0_PETBR	07YXO0	petaurus br
406	204	5.8	369	2	029128_9CHIR	029128	tonatia sau	479	184.5	5.3	565	2	04SOR9_TERNG	04SOR9	terracodon n
407	204	5.8	13100	2	009165_CAEEL	009165	caenorhabdi	480	184.5	5.3	643	2	018290_CAEEL	018290	caenorhabdi
408	203.5	5.8	405	2	09T142_EMBAT	09t142	emballonura	481	184.5	5.3	845	2	05VTE5_HUMAN	05VTE5	homo sapien
409	203.5	5.8	410	2	08M154_PIPAB	08m154	pipistrellu	482	184.5	5.3	3548	2	05VTE4_HUMAN	05VTE4	homo sapien
410	203.5	5.8	1180	1	ITAI1_RAT	09t142	emballonura	483	184.5	5.3	3574	2	04LDE5_HUMAN	04LDE5	homo sapien
411	203.5	5.8	2114	2	097267_PLAF7	097267	rattus norv	484	184	5.3	318	2	028341_CYNBP	028341	cynopterus
412	203	5.8	1019	2	06P001_HUMAN	06p001	homo sapien	485	184	5.3	445	2	06PCB0_HUMAN	06pcb0	homo sapien
413	202.5	5.8	322	2	07YXO0_DROAU	07yxo0	domomiciops	486	183.5	5.2	314	2	07YXO3_DASAL	07YXO3	dasyurus al
414	202.5	5.8	1332	2	09BPQ8_HALRO	09bpq8	halocynichia	487	183.5	5.2	319	2	03URV2_MOUSE	03URV2	mus musculus
415	202	5.8	139	2	04RVJ0_FELCA	04rvj0	tetracodon n	488	183.5	5.2	1165	1	ITAI1_BOVIN	ITAI1	bovin
416	202	5.8	403	2	02UY11_MOUSE	028410	felis silve	489	183.5	5.2	354	2	016003_HYDAT	016003	hydra atten
417	202	5.8	1141	2	05RL93_BRARE	05rl93	brachydanio	490	183	5.2	440	2	08CBT2_MOUSE	08CBT2	mus musculus
418	201.5	5.7	1168	2	091W4_MOUSE	091w4	mus musculus	491	182.5	5.2	848	2	08C720_MOUSE	08C720	mus musculus
419	200.5	5.7	406	2	091V61_PRODE	091v61	lophurromys	492	182.5	5.2	181	2	ITR2_HUMAN	ITR2	human
420	200	5.7	385	2	091U61_HUMAN	091u61	xenopus lae	493	182.5	5.2	367	2	09ES77_MOUSE	09ES77	mus musculus
421	200	5.7	425	2	09BDM6_HUMAN	09bdm6	homo sapien	494	182.5	5.2	357	2	07YXO2_ECHKA	07YXO2	echymipera
422	200	5.7	1014	2	05FWW2_XENLA	05fww2	homo sapien	495	181.5	5.2	415	2	0642A6_RAT	0642A6	rattus norv
423	200	5.7	1019	1	CO6A2_HUMAN	091w4	elephantinu	496	181.5	5.2	363	2	05G5W8_MACCG	05G5W8	macroderma
424	199.5	5.7	334	2	07YRM4_ELEED	07yrm4	elephantinu	497	181	5.2	1343	2	04TBJ2_TERNG	04TBJ2	tetracodon n
425	199.5	5.7	410	2	08WN33_9CHIR	08wn33	rhogessesa t	498	180.5	5.1	1614	2	04ZOP4_PLABE	04ZOP4	plasmodium
426	199.5	5.7	505	2	04SCD1_TERNG	04scd1	tetracodon n	499	179.5	5.1	326	2	08HXM7_GALPY	08HXM7	galenys pyr
427	199	5.7	407	2	07YRS6_TARBA	07yrs6	taraius ban	500	179	5.1	1196	2	098TF1_CYPCA	098TF1	cyprius ca
428	198.5	5.7	369	2	028340_CERST	028340	ceratotheri	501	179	5.1	1395	2	04XZL5_PLACH	04XZL5	plasmodium
429	198.5	5.7	369	2	028405_ELEUR	028405	elephantinu	502	178	5.1	763	2	031430_LAMJA	031430	lamia
430	198.5	5.7	682	2	03V391_MOUSE	03v391	mus musculus	503	177	5.1	422	2	08K118_DIPME	08K118	dipodomys m
431	198.5	5.7	1179	2	03V3R4_MOUSE	03v3r4	mus musculus	504	177	5.1	1009	2	04SNW2_TERNG	04SNW2	tetracodon n
432	198	5.7	406	2	028492_MEGLY	028492	megaderma t	505	177	5.1	1614	2	04ZOP4_PLABE	04ZOP4	plasmodium
433	197.5	5.6	322	2	07YQX8_9META	07yqx8	pseudochiro	506	176	5.0	1547	2	07RD70_PLAYO	07RD70	plasmodium
434	197.5	5.6	410	2	08M155_9CHIR	08m155	nyctalus av	507	175.5	5.0	1187	2	098TF0_CYPCA	098TF0	cyprius ca
435	196.5	5.6	415	2	08R225_MOUSE	08r225	mus musculus	508	175	5.0	310	2	09MZ67_GLOMA	09MZ67	globocephal
436	196.5	5.6	415	2	0923K3_MOUSE	0923k3	mus musculus	509	174.5	5.0	1016	2	061WN4_CAEBR	061WN4	caenorhabdi
437	196.5	5.6	1042	2	04RIX3_TERNG	04rix3	tetracodon n	510	173.5	5.0	418	2	03YVJ2_BIOGL	03YVJ2	biomphalari
438	195	5.6	752	2	04ROP0_TERNG	04rop0	tetracodon n	511	173	4.9	682	2	07YXK2_BOVIN	07YXK2	bov taureu
439	195	5.6	1160	2	09R200_MOUSE	09r200	mus musculus	512	172.5	4.9	364	2	019013_ERIEU	019013	erinaeus e
440	195	5.6	1161	2	03T9N8_MOUSE	03t9n8	mus musculus	513	172.5	4.9	418	2	03YVJ1_BIOGL	03YVJ1	biomphalari
441	195	5.6	1161	2	03T8B5_MOUSE	03t8b5	m b6-derive	514	172.5	4.9	565	2	06ZW26_HUMAN	06ZW26	homo sapien
442	195	5.6	1161	2	09WT4_MOUSE	09wt4	mus musculus	515	172.5	4.9	689	2	001545_CAEEL	001545	caenorhabdi
443	195	5.6	1162	2	03U159_MOUSE	03u159	mus musculus	516	172	4.9	336	2	05G5W7_ARTJA	05G5W7	artibeus ja
444	195	5.6	1163	1	ITAI1_MOUSE	p24063	mus musculus	517	171.5	4.9	1202	2	03U171_MOUSE	03U171	mus musculus
445	194	5.6	385	2	091V33_URARU	091v33	uratomys ru	518	171.5	4.9	1333	2	071442_CAEBR	071442	caenorhabdi
446	193.5	5.5	395	2	08HXM9_9EUTH	08hxm9	biariniella	519	171	4.9	712	2	043981_EIMTE	043981	eimeria ten
447	193.5	5.5	1172	2	03OK17_PIG	03ok17	sus scrofa	520	171	4.9	1045	2	0801S8_XENLA	0801S8	xenopus lae
448	193.5	5.5	1173	2	03OK18_PIG	03ok18	sus scrofa	521	170.5	4.9	615	2	060X10_CAEBR	060X10	caenorhabdi
449	193	5.5	422	2	08K116_THOTA	08k116	thomomys ta	522	170.5	4.9	1178	1	ITAI2_MOUSE	ITAI2	mouse
450	193	5.5	1151	1	ITAI1_HUMAN	p61199	homo sapien	523	170.5	4.9	1178	2	06PIC7_MOUSE	06PIC7	mus musculus
451	192.5	5.5	415	2	08C007_MOUSE	08c007	mus musculus	524	170	4.9	311	2	08MN36_9CHIR	08MN36	taphozous s
452	192.5	5.5	1168	1	ITAD_MOUSE	03v0c4	mus musculus	525	169	4.8	725	2	07YXK1_BOVIN	07YXK1	bov taureu
453	192.5	5.5	1189	1	ITAI1_HUMAN	03v0c4	mus musculus	526	168	4.8	202	2	04T1H8_TERNG	04T1H8	tetracodon n
454	192	5.5	108	2	04TER3_TERNG	04ter3	tetracodon n	527	167.5	4.8	304	2	06PG66_MOUSE	06PG66	mus musculus
455	192	5.5	1164	2	04QWZ3_SHEEP	04qwz3	ovis aries	528	167.5	4.8	323	2	08CB84_MOUSE	08CB84	mus musculus
456	192	5.5	1165	2	04QWZ2_SHEEP	04qwz2	ovis aries	529	167.5	4.8	324	2	08S017_MICLA	08S017	microptero
457	191.5	5.5	599	2	08WQ1_9ASCI	08wq1	bolientia vi	530	167.5	4.8	552	2	04NP22_THEPA	04NP22	thelateria p
458	191.5	5.5	1388	2	07TQC3_MOUSE	07tqc3	mus musculus	531	167.5	4.8	1167	1	ITAE_MOUSE	ITAE	mouse
459	191	5.5	329	2	07YRM7_ELEMY	07yrm7	elephantinu	532	167	4.8	630	2	029124_PIG	029124	caenorhabdi
460	191	5.5	403	2	05G5W5_THYTR	05g5w5	thyroptera	533	166.5	4.8	319	2	08HXM6_9EUTH	08HXM6	uroisipus s
461	190.5	5.4	205	2	063001_RAT	063001	rattus norv	534	166.5	4.8	191	2	029124_PIG	029124	caenorhabdi
462	190.5	5.4	833	2	096442_STRPU	096442	strongyloce	535	166.5	4.8	487	2	09HOB8_HUMAN	09HOB8	homo sapien
463	190	5.4	411	2	09XSA1_HIPAM	09xsa1	hippocamu	536	166.5	4.8	889	2	05GCC1_CARRO	05GCC1	carinascor
464	190	5.4	1164	2	032Y14_CAPIH	032y14	capra hircu	537	166.5	4.8	1160	2	08MKF4_FELCA	08MKF4	felis silve
465	190	5.4	1165	2	032Y13_CAPIH	032y13	capra hircu	538	166	4.7	314	2	05G5W6_ANOGE	05G5W6	anoura geof
466	189.5	5.4	1905	2	09XTP6_PLABE	09xtp6	plasmodium	539	166	4.7	394	2	08IRG8_BIOGL	08IRG8	biomphalari
467	189	5.4	1160	2	03T116_RAT	03t116	rattus norv	540	165.5	4.7	1038	2	08BS01_MOUSE	08BS01	mus musculus
468	188.5	5.4	285	1	ITAI1_CHICK	090615	gallus gall	541	165.5	4.7	1167	2	05SRV0_MOUSE	05SRV0	mus musculus
469	188.5	5.4	322	2	07YXK1_9META	07yqx1	rhyncholest	542	165	4.7	333	2	05G5W3_EUDAU	05G5W3	eunops auri

543	165	4.7	1031	2	Q4SHJ3_TETNG	Q4shj3 tetradon n	616	139	4.0	676	2	Q5F3F4_CHICK	Q5f3f4 gallus galli
544	165	4.7	1247	2	Q5CLR6_CRYHO	Q5clr6 cryptospori	617	138.5	4.0	747	2	Q6NM57_BRARE	Q6nm57 brachydanio
545	165	4.7	1247	2	Q5CU06_CRYPV	Q5cu06 cryptospori	618	138	3.9	436	2	Q951L5_MACFA	Q951l5 macaca fasc
546	164.5	4.7	633	2	Q4SVDP_TETNG	Q4svdp tetradon n	619	138	3.9	923	2	Q5AUS9_EMENT	Q5aus9 emment
547	164.5	4.7	895	2	Q9WUP8_9MURI	Q9wup8 mus sp. itg	620	137.5	3.9	406	2	Q9TV40_TRADR	Q9tv40 tradra
548	164.5	4.7	1166	2	Q3U4V9_MOUSE	Q3u4v9 mus musculu	621	137	3.9	744	2	Q5SK30_CRYNE	Q5sk30 cryptococcu
549	164.5	4.7	1167	2	Q8B340_RAT	Q8b340 rattus norv	622	136.5	3.9	1601	2	Q4UEZ8_THEAN	Q4uez8 thelleria a
550	163.5	4.7	765	2	Q9U8J9_NEOCA	Q9u8j9 neospora ca	623	136	3.9	1779	2	Q61X39_CAEBR	Q61x39 caenorhabd
551	163.5	4.7	1280	2	Q3S621_TOXGO	Q3s621 toxoplasma	624	135.5	3.9	577	2	Q5GZ84_XANOR	Q5gz84 xenothoma sp
552	163	4.7	1086	2	Q96HB1_HUMAN	Q96hb1 homo sapien	625	135.5	3.9	833	2	Q8YUR6_ANASP	Q8yur6 anabomna sp
553	162.5	4.6	497	2	Q6UWH0_HUMAN	Q6uwh0 homo sapien	626	135	3.9	1234	2	Q4YBD6_PLACH	Q4ybd6 plasmodium
554	162.5	4.6	1179	1	ITPE_HUMAN	ITPEsm7 homo sapien	627	135	3.9	1304	2	Q8WTE3_PLABE	Q8wte3 plasmodium
555	161.5	4.6	305	2	Q7YQX4_9META	Q7yqx4 smmthopis	628	134.5	3.8	403	2	Q8WY04_BRARE	Q8wy04 brachydanio
556	160.5	4.6	1167	2	Q8B341_RAT	Q8b341 rattus norv	629	134.5	3.8	921	2	Q921U8_MOUSE	Q921u8 mus musculu
557	160	4.6	473	2	Q4SMW7_TETNG	Q4smw7 tetradon n	630	134	3.8	1246	2	Q3S622_TOXGO	Q3s622 toxoplasma
558	160	4.6	1083	2	Q26423_CARRO	Q26423 carcinoscor	631	134	3.8	12268	2	Q8M008_CAEBL	Q8m008 caebell
559	159.5	4.6	1019	1	LFC_CARRO	LFC c. limulus c	632	133.5	3.8	577	2	Q2P234_XANOR	Q2p234 xanor
560	159.5	4.6	1019	1	LFC_TACTR	LFC tachypleus	633	133.5	3.8	715	1	DCBD1_HUMAN	DCBD1 human
561	159.5	4.6	1019	1	Q8T9S1_TACTR	Q8t9s1 tachypleus	634	133	3.8	234	2	Q405F1_9RHOB	Q405f1 9rhob
562	159	4.6	769	2	Q00816_TOXGO	Q00816 toxoplasma	635	133	3.8	683	2	Q2UA88_ASFOR	Q2ua88 aspergillus
563	159	4.5	1969	2	Q69HL6_CIOIN	Q69hl6 ciona intes	636	132.5	3.8	244	2	Q2VCM5_9CARN	Q2vcn5 vulpes cana
564	158.5	4.5	156	2	Q71V33_HUMAN	Q71v33 homo sapien	637	132.5	3.8	921	2	Q8CD93_MOUSE	Q8cd93 mus musculu
565	157.5	4.5	293	2	Q7YQX5_PHTATA	Q7yqx5 phascogale	638	132.5	3.8	1063	2	Q81WR4_HUMAN	Q81wr4 human
566	157.5	4.5	1451	2	Q5CNE9_CRYHO	Q5cne9 cryptospori	639	132.5	3.8	1063	2	Q8N406_HUMAN	Q8n406 human
567	157	4.5	516	2	Q5TDB6_HUMAN	Q5tdb6 homo sapien	640	132	3.8	920	2	Q6NSW1_MOUSE	Q6nsw1 mus musculu
568	156.5	4.5	494	2	Q3U4C7_MOUSE	Q3u4c7 mus musculu	641	132	3.8	1247	2	Q817Z6_TOXGO	Q817z6 toxoplasma
569	156.5	4.5	494	2	Q9D2R3_MOUSE	Q9d2r3 m 10 day ol	642	131.5	3.8	241	2	Q99806_HUMAN	Q99806 homo sapien
570	156.5	4.5	495	2	Q8B2Q2_MOUSE	Q8b2q2 mus musculu	643	131.5	3.8	244	2	Q2VCL9_VITLZE	Q2vcl9 vulpes zerd
571	156	4.5	427	2	Q6OR12_CAEBR	Q6or12 caenorhabd	644	131.5	3.8	244	2	Q2VCM0_VUUYU	Q2vcn0 vulpes vulp
572	156	4.5	523	2	Q9B8T5_CHICK	Q9b8t5 gallus galli	645	131.5	3.8	244	2	Q2VCN1_9CARN	Q2vcn1 vulpes cana
573	155.5	4.4	1556	2	Q61139_CRYPV	Q61139 cryptospori	646	131.5	3.8	244	2	Q2VCM2_VULMA	Q2vcn2 vulpes macr
574	155	4.4	358	2	Q29134_TUPGL	Q29134 tupala glis	647	131.5	3.8	244	2	Q2VCM3_9CARN	Q2vcn3 vulpes cors
575	155	4.4	686	2	Q4WEG9_ASPFU	Q4weg9 aspergillus	648	131.5	3.8	244	2	Q2VCP8_ALOLA	Q2vcp8 aspergillus
576	155	4.4	1272	2	Q81M24_PLAF7	Q81m24 plasmodium	649	131.5	3.8	328	2	Q3IEE7_PSEHT	Q3iee7 pseudox lago
577	155	4.4	1674	2	Q5CZ08_CRYPV	Q5cz08 cryptospori	650	131.5	3.8	533	2	Q94677_PLACN	Q94677 plasmodium
578	154.5	4.4	2482	2	Q61GPR_CAEBR	Q61gpr caenorhabd	651	131.5	3.8	572	2	Q9G5R0_PLACN	Q9g5r0 plasmodium
579	153.5	4.4	425	2	Q9GZFS_CAEBL	Q9gzfs caenorhabd	652	131.5	3.8	713	2	Q6GL27_XENTR	Q6gl27 xenopus tiro
580	153	4.4	393	2	Q4TU50_NECAM	Q4tu50 necator ame	653	131	3.7	959	2	Q05504_MOUSE	Q05504 mus musculu
581	152	4.3	449	2	Q6P590_HUMAN	Q6p590 homo sapien	654	130.5	3.7	240	2	Q2VCM2_PSEGR	Q2vcn2 pseudalopex
582	152	4.3	500	2	Q4V9V5_XENTR	Q4v9v5 xenopus tiro	655	130.5	3.7	244	2	Q2VCM9_PSEVE	Q2vcn9 pseudalopex
583	151.5	4.3	1117	2	Q4RXN8_TETNG	Q4rxn8 tetradon n	656	130.5	3.7	244	2	Q2VCM9_PSEVE	Q2vcn9 pseudalopex
584	151.5	4.3	1556	2	Q5CJ50_CRYHO	Q5cj50 cryptospori	657	130.5	3.7	713	2	Q6GN18_XENLA	Q6gn18 xenopus lae
585	150.5	4.3	724	2	Q04388_ETMMA	Q04388 etimelia max	658	130	3.7	146	2	Q06930_PLAPA	Q06930 plasmodium
586	150.5	4.3	813	2	Q4XSS2_PLACH	Q4xss2 plasmodium	659	130	3.7	639	2	Q6K825_ORYSA	Q6k825 oryza sativ
587	149.5	4.3	784	2	Q2SV15_BURTH	Q2sv15 burkholderi	660	129.5	3.7	244	2	Q2VCM6_9CARN	Q2vcn6 urocyon lit
588	149.5	4.3	1167	1	ITAI10_HUMAN	ITAI10 homo sapien	661	129.5	3.7	703	2	Q8N1Y7_NEUCR	Q8n1y7 neurospora
589	149	4.3	903	2	Q464T6_THEAN	Q464t6 thelleria a	662	129	3.7	482	2	Q8NA36_HUMAN	Q8na36 homo sapien
590	148	4.2	1615	2	Q7RQW4_PLAYO	Q7rqw4 plasmodium	663	129	3.7	1251	2	Q4SQ95_TETNG	Q4sq95 tetradon n
591	147.5	4.2	406	2	Q28638_GALCR	Q28638 galago cras	664	129	3.7	1784	2	Q9VE02_DROME	Q9ve02 drosophila
592	146.5	4.2	767	2	Q8RTW1_CLODI	Q8rtcw1 clostridium	665	128.5	3.7	244	2	Q2VCM8_SPEVE	Q2vcn8 speocheos ve
593	146.5	4.2	2359	2	Q4SOB4_TETNG	Q4sob4 tetradon n	666	128.5	3.7	244	2	Q2VCM0_PSEBU	Q2vcn0 pseudalopex
594	146	4.2	1304	2	Q4YUE0_PLABE	Q4yue0 plasmodium	667	128.5	3.7	244	2	Q2VCN1_PSEBY	Q2vcn1 pseudalopex
595	145	4.1	1613	2	Q4N5G4_THEPA	Q4n5g4 thelleria p	668	128.5	3.7	244	2	Q2VCN3_9CARN	Q2vcn3 pseudalopex
596	144.5	4.1	606	2	Q464T5_THEAN	Q464t5 thelleria a	669	128.5	3.7	244	2	Q2VCN9_CHRBR	Q2vcn9 chrysocyon
597	143.5	4.1	1701	2	Q8K018_MOUSE	Q8k018 mus musculu	670	128.5	3.7	244	2	Q2VCP7_ATEMI	Q2vcp7 atelocynus th
598	143.5	4.1	500	2	Q9H336_HUMAN	Q9h336 homo sapien	671	128.5	3.7	244	2	Q2VCP0_DUSTH	Q2vcp0 diacyclops
599	143.5	4.1	767	2	Q8CGD2_MOUSE	Q8cgd2 m. cocoacris	672	128.5	3.7	266	2	Q8C6P0_MOUSE	Q8c6p0 mus musculu
600	143.5	4.1	500	2	Q2N3V5_CLODI	Q2n3v5 clostridium	673	128.5	3.7	531	2	Q4V6F8_PLACH	Q4v6f8 plasmodium
601	143	4.1	931	2	Q4N102_THEPA	Q4n102 thelleria p	674	128.5	3.7	614	2	Q8VNU9_LACLU	Q8vnu9 lacobacilli
602	143	4.1	1530	2	Q7RP79_PLAYO	Q7rp79 plasmodium	675	128.5	3.7	845	2	Q8WU03_PLACH	Q8wu03 plasmodium
603	142	4.1	106	2	Q4Y3E4_PLACH	Q4y3e4 plasmodium	676	128.5	3.7	921	2	Q9R0D0_MOUSE	Q9r0d0 mus musculu
604	142	4.1	655	2	Q6UJH3_BABBO	Q6ujh3 babezia bov	677	128.5	3.7	923	2	Q9R2S3_MOUSE	Q9r2s3 mus musculu
605	142	4.1	744	2	Q5KR9G_CRYNE	Q5kr9g cryptococcu	678	128.5	3.7	1235	2	Q659T9_CIOIN	Q659t9 ciona intes
606	141.5	4.0	2938	2	Q61769_MOUSE	Q61769 mus musculu	679	128	3.7	909	2	Q2Z1I5_CALSA	Q2z1i5 caldicellul
607	141	4.0	371	2	Q96K61_HUMAN	Q96k61 homo sapien	680	128	3.7	1200	1	HYAL_STRPU	Q76536 strongyloce
608	141	4.0	1562	2	Q5UWJ9_HALMA	Q5uwj9 haloarcula	681	127.5	3.6	244	2	Q2VCN5_OTOME	Q2vcn5 otocyon meg
609	140.5	4.0	429	2	Q7I6430_CAEBL	Q7i6430 caenorhabd	682	127.5	3.6	429	2	Q61RCS_CAEBR	Q61rccs caenorhabd
610	140.5	4.0	449	2	Q7IUN8_CAEBL	Q7iun8 caenorhabd	683	127.5	3.6	641	2	Q8BVW2_MOUSE	Q8bvww2 mus musculu
611	140.5	4.0	921	2	Q3TCV2_MOUSE	Q3tcv2 mus musculu	684	127.5	3.6	1061	2	Q69YK7_HUMAN	Q69yk7 homo sapien
612	140	4.0	478	2	Q61PA3_CAEBR	Q61pa3 caenorhabd	685	127.5	3.6	1103	2	Q9CAJ7_NEUCR	Q9caj7 neurospora
613	139.5	4.0	614	2	Q94674_PLAGA	Q94674 plasmodium	686	127.5	3.6	1837	2	Q9N5F6_CAEBL	Q9n5f6 caenorhabd
614	139	4.0	503	1	DCBD1_MOUSE	Q944j3 mus musculu	687	127	3.6	419	1	RD23C_ARATH	Q841j1 arabidopsis
615	139	4.0	507	2	Q99MW6_MOUSE	Q99mwe mus musculu	688	127	3.6	1434	2	Q6NP25_DROME	Q6np25 drosophila

689	127	3.6	1766	2	Q2U7Y5_ASPOR	Q2U7Y5_aspergillus	762	121.5	3.5	903	1	EC1C_BOVIN	P54281_bos_taurus
690	127	3.6	1832	2	Q4PF70_USTMA	Q4PF70_ustilaago ma	763	121.5	3.5	1497	2	Q7USA4_RHOBA	Q7USA4_rhodospirillum rubrum
691	126.5	3.6	244	2	Q2VCN7_LYCPI	Q2VCN7_lyciaan pict	764	121.5	3.5	2522	2	Q8EKA6_SHEON	Q8EKA6_sheonanella
692	126.5	3.6	244	2	Q2VCN8_CUOAI	Q2VCN8_cuon alpinu	765	121	3.5	509	2	Q3F4N3_9BURK	Q3F4N3_burkholderia
693	126.5	3.6	244	2	Q2VCP1_CANSI	Q2VCP1_canis salmen	766	121	3.5	556	2	Q964S6_PLAVI	Q964S6_plasmodium
694	126.5	3.6	244	2	Q2VCP2_3CARN	Q2VCP2_canis mesom	767	121	3.5	556	2	Q91VF0_PLAVI	Q91VF0_plasmodium
695	126.5	3.6	244	2	Q2VCP6_CANAD	Q2VCP6_canis adust	768	121	3.5	1153	1	MAMU2_HUMAN	Q81512_homo_sapien
696	126.5	3.6	328	2	Q2PFU5_MACFA	Q2PFU5_macaca fasc	769	121	3.5	1159	2	Q7U7U9_SYNPX	Q7U7U9_synechococcus
697	126.5	3.6	454	2	Q9X7Q9_CAEEL	Q9X7Q9_caenorhabdi	770	121	3.5	1232	2	Q68219_ANAPH	Q68219_anaplaasma p
698	126.5	3.6	669	2	Q4SH26_TETNG	Q4SH26_tetradodon n	771	121	3.5	1232	2	Q9UR07_ANAPH	Q9UR07_anaplaasma p
699	126.5	3.6	683	2	Q2KAB7_RHIER	Q2KAB7_rhizobium e	772	121	3.5	1598	2	Q60RK8_CARRR	Q60RK8_caenorhabdi
700	126.5	3.6	775	1	DEBD2_HUMAN	Q66P2_homo sapien	773	120.5	3.4	630	2	Q2W329_MAGSA	Q2W329_magnetospirillum
701	126	3.6	588	2	Q53OF6_HUMAN	Q53QF6_homo sapien	774	120.5	3.4	929	2	Q64ZU1_MOUSE	Q64ZU1_mus musculus
702	126	3.6	664	2	Q91NG4_ARATH	Q91NG4_arabidopsis	775	120.5	3.4	964	1	MK11_MOUSE	Q84316_mus musculus
703	126	3.6	800	2	Q4Y340_PLACH	Q4Y340_plasmodium	776	120.5	3.4	964	2	Q3U1I6_MOUSE	Q3U1I6_mus musculus
704	126	3.6	805	2	Q66KFO_XENLA	Q66KFO_xenopus lae	777	120.5	3.4	1135	2	Q6BXC0_DEBHA	Q6BXC0_debaryomyces
705	126	3.6	1649	2	Q57UM9_9TRYP	Q57UM9_tyrpanosoma	778	120.5	3.4	1435	2	Q4NZY3_THRPA	Q4NZY3_thelateria p
706	126	3.6	1649	2	Q8MBB3_3TRYP	Q8MBB3_tyrpanosoma	779	120.5	3.4	2013	2	Q8YPT8_LISMO	Q8YPT8_leishmania
707	126	3.6	3529	2	Q4N9U4_THRPA	Q4N9U4_thelateria p	780	120	3.4	158	2	Q4XHB8_PLACH	Q4XHB8_plasmodium
708	126	3.6	3529	2	Q9GP30_THRPA	Q9GP30_thelateria p	781	120	3.4	510	2	Q94727_PLAVI	Q94727_plasmodium
709	125.5	3.6	244	2	Q2VCM4_VULCH	Q2VCM4_vulpes cham	782	120	3.4	573	1	MUC13_MOUSE	P19467_mus musculus
710	125.5	3.6	661	2	Q21394_CAEEL	Q21394_caenorhabdi	783	120	3.4	573	2	Q3V1S6_MOUSE	Q3V1S6_mus musculus
711	125.5	3.6	1044	2	Q4AB30_DROME	Q4AB30_drosophila	784	120	3.4	747	2	Q7UML2_RHOBA	Q7UML2_rhodospirillum
712	125.5	3.6	1283	1	RF1P1_HUMAN	Q6WK2_homo sapien	785	120	3.4	922	2	Q6MTH5_BDEBA	Q6MTH5_bdellovibrio
713	125.5	3.6	1788	2	Q9VE13_DROME	Q9VE13_drosophila	786	120	3.4	939	2	Q8YGR3_ANNAP	Q8YGR3_anabaena bp
714	125	3.6	478	2	Q33082_MYCLE	Q33082_mycobacteri	787	119.5	3.4	123	2	Q41I29_TETNG	Q41I29_tetradodon n
715	125	3.6	586	2	Q9CDD8_MYCLE	Q9CDD8_mycobacteri	788	119.5	3.4	369	2	Q7VTP2_BORPE	Q7VTP2_borrelia
716	125	3.6	769	1	DCBD2_RAT	Q91VZ_rattus norv	789	119.5	3.4	468	2	Q55279_ADEGX	Q55279_avian adeno
717	125	3.6	1272	2	Q2U4F6_ASPOR	Q2U4F6_aspergillus	790	119.5	3.4	728	2	Q4OFZ3_LEIMA	Q4OFZ3_leishmania
718	125	3.6	1426	2	Q9X3P6_9FIRM	Q9X3P6_caldicellul	791	119.5	3.4	838	2	Q3MH16_ANNAT	Q3MH16_anabaena va
719	125	3.6	2207	2	Q42619_DESHA	Q42619_desulfotoba	792	119.5	3.4	1151	2	Q6CMS9_KUDIA	Q6CMS9_kluyveromyces
720	124.5	3.6	244	2	Q2VCW7_UROCI	Q2VCW7_urocyon cin	793	119.5	3.4	1216	2	Q551S2_CRYNE	Q551S2_cryptococcus
721	124.5	3.6	602	2	Q9Y092_DROME	Q9Y092_drosophila	794	119.5	3.4	1216	2	Q5KXC7_CRYNE	Q5KXC7_cryptococcus
722	124.5	3.6	925	1	NPAC2_HUMAN	Q13469_homo sapien	795	119.5	3.4	1456	2	Q8V967_PVX	Q8V967_potato_viru
723	124.5	3.6	1001	2	Q6K9R1_ORYSA	Q6K9R1_oryza sativ	796	119.5	3.4	22152	2	Q8WKT7_HUMAN	Q8WKT7_homo sapien
724	124.5	3.6	1608	2	Q8T5Z6_PLABE	Q8T5Z6_plasmodium	797	119	3.4	393	2	Q9S572_DROME	Q9S572_drosophila
725	124.5	3.6	1634	2	Q4YWS7_PLABE	Q4YWS7_plasmodium	798	119	3.4	547	2	Q41700_GIBZE	Q41700_gibberella
726	124	3.5	225	2	Q5EBB8_RAT	Q5EBB8_rattus norv	799	119	3.4	725	1	AGAL_YEAST	P32223_saccharomyces
727	124	3.5	572	2	Q9RC13_LACDL	Q9RC13_lactobacill	800	119	3.4	1328	1	AGRN_DISTOM	Q90404_discofrype o
728	124	3.5	617	2	Q43NM2_SOLUS	Q43NM2_solibacter	801	119	3.4	1588	2	Q7DJ60_ECOS7	Q7DJ60_escherichia
729	124	3.5	769	1	DCBD2_MOUSE	Q91VZ3_mus musculu	802	118.5	3.4	143	2	Q7J173_BOVIN	Q7J173_bos taurus
730	124	3.5	892	2	Q41P94_METBU	Q41P94_methanococc	803	118.5	3.4	237	2	P79296_PIG	P79296_pis scrofa
731	123.5	3.5	244	2	Q2VCN6_NYCPR	Q2VCN6_nycteraleus	804	118.5	3.4	571	2	Q8G9M0_RHOBA	Q8G9M0_rhodococcus
732	123.5	3.5	697	2	Q4DZP3_TRYCR	Q4DZP3_tyrpanosoma	805	118.5	3.4	582	2	Q82P59_STRAW	Q82P59_striptomyces
733	123.5	3.5	1456	2	Q9JEX8_PVX	Q9JEX8_potato_viru	806	118.5	3.4	627	1	Q6UDM8_TREBE	Q6UDM8_trepionema 1
734	123.5	3.5	1628	2	Q4U9S5_THRAN	Q4U9S5_thelateria a	807	118.5	3.4	785	1	CADH7_CHICK	Q90763_gallus gall
735	123	3.5	501	2	Q41MR7_GIBZE	Q41MR7_gibberella	808	118.5	3.4	1409	2	Q5ALTS_CANAL	Q5ALTS_candida alb
736	123	3.5	426	2	Q4STC6_TETNG	Q4STC6_tetradodon n	809	118.5	3.4	1689	2	Q91IR1_9VTRU	Q91IR1_crimnear-con
737	123	3.5	740	2	Q41AK6_TETNG	Q41AK6_tetradodon n	810	118.5	3.4	2013	2	Q4E0Y1_LISMO	Q4E0Y1_listeria mo
738	123	3.5	1143	2	Q40ZU6_9FIRM	Q40ZU6_eubacterium	811	118.5	3.4	4104	2	Q36B39_9GAMM	Q36B39_shevanella
739	123	3.5	1203	2	Q9N5K0_CAEEL	Q9N5K0_caenorhabdi	812	118	3.4	508	2	Q39DH7_BURS3	Q39DH7_burkholderi
740	123	3.5	2375	2	Q581L4_9CAUD	Q581L4_cyanophaga	813	118	3.4	555	2	Q7XXL2_ORYSA	Q7XXL2_oryza sativ
741	123	3.5	8682	2	Q88RG2_PSEPK	Q88RG2_pseudomonas	814	118	3.4	583	2	Q7XUX2_ORYSA	Q7XUX2_oryza sativ
742	122.5	3.5	244	2	Q2VCP5_CANAU	Q2VCP5_canis aureu	815	118	3.4	609	2	Q8FMS3_CORRE	Q8FMS3_corynebacte
743	122.5	3.5	552	2	Q3SX17_HUMAN	Q3SX17_homo sapien	816	118	3.4	812	2	Q6C8U0_YARLI	Q6C8U0_yarrowia 11
744	122.5	3.5	633	2	Q4CQF5_TRYCR	Q4CQF5_tyrpanosoma	817	118	3.4	1050	2	Q5EWX9_XENLA	Q5EWX9_xenopus lae
745	122.5	3.5	657	2	Q4MUU0_ASPFU	Q4MUU0_aspergillus	818	118	3.4	2733	2	Q9J3E8_9CORO	Q9J3E8_murine hepa
746	122.5	3.5	932	2	Q6K4C3_ORYSA	Q6K4C3_oryza sativ	819	117.5	3.4	915	2	Q8WMM2_HUMAN	Q8WMM2_homo sapien
747	122.5	3.5	1458	2	Q757N5_ASHGO	Q757N5_ashbya gos	820	117.5	3.4	917	1	SMOO_HUMAN	P53114_homo sapien
748	122.5	3.5	1472	2	Q4YAV8_PLABE	Q4YAV8_plasmodium	821	117.5	3.4	940	2	Q8WMM1_HUMAN	Q8WMM1_homo sapien
749	122.5	3.5	1744	2	Q82YV8_ENTPA	Q82YV8_enterococcu	822	117.5	3.4	1312	2	Q9U113_LEIMA	Q9U113_leishmania
750	122.5	3.5	1814	1	TSC2_MOUSE	Q61037_mus musculu	823	117.5	3.4	1424	2	Q5K868_CRYNE	Q5K868_cryptococcus
751	122.5	3.5	1844	2	Q22579_CAEEL	Q22579_caenorhabdi	824	117.5	3.4	1456	2	Q400L3_PVX	Q400L3_potato_viru
752	122	3.5	545	2	Q44019_GAPIC	Q44019_plasmodium	825	117.5	3.4	1808	2	Q3UHB2_MOUSE	Q3UHB2_mus musculu
753	122	3.5	566	2	Q5CKZ9_CRYHO	Q5CKZ9_cryptospori	826	117	3.3	552	2	Q3BBQ7_RAT	Q3BBQ7_rattus norv
754	122	3.5	1046	2	Q4SMK2_TETNG	Q4SMK2_tetradodon n	827	117	3.3	654	2	Q4PRL8_USYMA	Q4PRL8_ustilaago ma
755	122	3.5	1409	2	Q5SMK2_CRYNE	Q5SMK2_cryptococcu	828	117	3.3	795	2	Q5NM24_9ARCH	Q5NM24_uncultured
756	122	3.5	1595	2	Q52373_9TRIM	Q52373_caldicellul	829	117	3.3	939	2	Q3WCU4_ANNAT	Q3WCU4_anabaena va
757	121.5	3.5	244	2	Q2VCP3_CANTU	Q2VCP3_canis lupus	830	117	3.3	1205	2	Q56A66_XENLA	Q56A66_xenopus lae
758	121.5	3.5	244	2	Q2VCP4_CANTU	Q2VCP4_canis latra	831	117	3.3	1213	2	Q7SEF98_NEUCR	Q7SEF98_neurospora
759	121.5	3.5	253	2	Q8WMM5_RHITA	Q8WMM5_rhizopoma h	832	117	3.3	1836	2	Q9LXK4_ARATH	Q9LXK4_arabidopsis
760	121.5	3.5	253	2	Q9U8H1_GAPIC	Q9U8H1_plasmodium	833	117	3.3	2154	2	Q4NBD2_THRPA	Q4NBD2_thelateria p
761	121.5	3.5	858	2	Q7R0S5_PLAVO	Q7R0S5_plasmodium	834	117	3.3	2221	2	Q4SEB0_TETNG	Q4SEB0_tetradodon n

835	117	3.3	2503	2	Q99136_PRRSV	Q99136	porcine rep	908	114	3.3	1088	2	Q5R161_BRARE	Q5R161	brachydanio
836	116.5	3.3	756	2	Q8B9X1_XANAC	Q8B9X1	xanthomonas	909	114	3.3	1431	1	CSK11_HUMAN	CSK11	human
837	116.5	3.3	575	2	Q9AEM3_CLODI	Q9AEM3	cloditium	910	114	3.3	1625	1	Q6WV4_NEUCR	Q6WV4	neurospora
838	116.5	3.3	938	1	SEY1_YARLI	SEY1	yarlowia li	911	114	3.3	1752	2	Q7R1Y7_GIALA	Q7R1Y7	giala
839	116.5	3.3	989	2	Q5NG27_ZYMO	Q5NG27	zymomonas m	912	114	3.3	2308	2	Q83N13_TROWA	Q83N13	trowa
840	116.5	3.3	3300	2	Q4N127_THERA	Q4N127	thellieria p	913	114	3.3	2308	2	Q83N13_TROWA	Q83N13	trowa
841	116.5	3.3	4567	2	Q36C93_9GAM	Q36C93	shewanella	914	114	3.3	5017	2	Q4U64_THEAN	Q4U64	thean
842	116	3.3	299	2	Q3EBD0_ARATH	Q3EBD0	arabidopsis	915	113.5	3.2	480	2	Q81SNO_BACAN	Q81SNO	bacan
843	116	3.3	487	1	Q3TRC6_MOUSE	Q3TRC6	mus musculus	916	113.5	3.2	557	2	Q91SK7_ARATH	Q91SK7	arath
844	116	3.3	487	2	Q3TRC6_MOUSE	Q3TRC6	mus mod-deriv	917	113.5	3.2	557	2	Q4R7B7_MACFA	Q4R7B7	macfa
845	116	3.3	558	2	Q6MZG6_HUMAN	Q6MZG6	homo sapien	918	113.5	3.2	660	2	Q5L4M1_GVIRU	Q5L4M1	gviru
846	116	3.3	629	2	Q2TY93_ASPOR	Q2TY93	aspergillus	919	113.5	3.2	725	2	Q54B41_DICDI	Q54B41	dicdi
847	116	3.3	629	2	Q4SUQ4_TETNG	Q4SUQ4	tetradodon n	920	113.5	3.2	716	2	Q3CR57_ALTAT	Q3CR57	altat
848	116	3.3	775	1	TAU_HYLA	TAU	hylobates l	921	113.5	3.2	815	2	Q8N536_HUMAN	Q8N536	human
849	116	3.3	775	1	Q5CZ17_HUMAN	Q5CZ17	homo sapien	922	113.5	3.2	951	2	Q9GLY4_RABIT	Q9GLY4	rabit
850	116	3.3	1043	1	GRIP2_RAT	GRIP2	rattus norv	923	113.5	3.2	1123	2	Q5T0Z1_ANOGA	Q5T0Z1	anoga
851	116	3.3	1053	2	Q2R2P2_ORYSA	Q2R2P2	oryza sativ	924	113.5	3.2	1153	2	Q80T83_MOUSE	Q80T83	mouse
852	116	3.3	1161	2	Q7RVQ2_NEUCR	Q7RVQ2	neurospora	925	113.5	3.2	1159	2	Q4UDB8_THEAN	Q4UDB8	thean
853	116	3.3	1292	2	Q6C8B9_YARLI	Q6C8B9	yarlowia li	926	113.5	3.2	1660	2	Q39KNO_LEIMA	Q39KNO	leima
854	116	3.3	1562	2	Q3MP25_CANAL	Q3MP25	candida alb	927	113.5	3.2	1673	2	Q39E59_BUR83	Q39E59	bur83
855	116	3.3	7176	1	RIAB_CVMA5	RIAB	m replicase	928	113.5	3.2	1982	2	Q86JD5_DICDI	Q86JD5	dicdi
856	116	3.3	7178	1	Q66W16_9COCO	Q66W16	murine hepa	929	113.5	3.2	2026	2	Q551R4_DICDI	Q551R4	dicdi
857	115.5	3.3	428	1	ELK1_HUMAN	ELK1	homo sapien	930	113.5	3.2	2186	2	Q54ZM9_DICDI	Q54ZM9	dicdi
858	115.5	3.3	428	2	Q6FG56_HUMAN	Q6FG56	homo sapien	931	113.5	3.2	2528	2	Q86JD6_DICDI	Q86JD6	dicdi
859	115.5	3.3	454	2	Q6S8R6_HUMAN	Q6S8R6	homo sapien	932	113.5	3.2	507	2	Q59G82_HUMAN	Q59G82	human
860	115.5	3.3	549	2	Q6AEJ9_LEIXX	Q6AEJ9	leifsonia x	933	113	3.2	565	2	Q4CG76_CLOTM	Q4CG76	clotm
861	115.5	3.3	614	2	Q3FB42_9BURK	Q3FB42	burkholderi	934	113	3.2	771	2	Q22783_CAEEL	Q22783	caeel
862	115.5	3.3	688	2	Q4YV42_PLABE	Q4YV42	plasmidemia	935	113	3.2	775	1	TAU_GORGO	TAU	gorgo
863	115.5	3.3	1016	2	Q4HW12_GIBZE	Q4HW12	gibberella	936	113	3.2	775	1	TAU_PANTR	TAU	pantr
864	115.5	3.3	1430	1	CSK11_RAT	CSK11	rattus norv	937	113	3.2	839	1	Q55C56_DICDI	Q55C56	dicdi
865	115.5	3.3	2186	2	Q8NW19_STEAM	Q8NW19	staphylococ	938	113	3.2	882	2	Q3GB24_9FIRM	Q3GB24	9firm
866	115.5	3.3	2800	2	Q6XHB1_DICDI	Q6XHB1	dictyosteli	939	113	3.2	912	2	Q5B926_EMENT	Q5B926	ement
867	115	3.3	595	1	THD1_LYCES	THD1	lycopersico	940	113	3.2	980	2	Q7XERTS_ORYSA	Q7XERTS	orysa
868	115	3.3	659	2	Q3JN26_BURP1	Q3JN26	burkholderi	941	113	3.2	1405	2	Q54GM9_DICDI	Q54GM9	dicdi
869	115	3.3	843	2	Q35CD8_9BRAD	Q35CD8	bradyrhizob	942	113	3.2	1984	2	Q4M001_ASPRU	Q4M001	aspru
870	115	3.3	1091	2	Q3BFS8_EMENT	Q3BFS8	aspergillus	943	113	3.2	3956	2	Q9DLN9_PRRSV	Q9DLN9	prrrsv
871	115	3.3	1096	2	Q3PH67_PARDE	Q3PH67	paracoccus	944	112.5	3.2	289	2	Q2R2G3_9SPHI	Q2R2G3	9spphi
872	115	3.3	1262	2	Q4HYB2_GIBZE	Q4HYB2	shewanella	945	112.5	3.2	386	2	Q40854_9RHOB	Q40854	9rhob
873	115	3.3	1262	2	Q2ZA32_9GAMM	Q2ZA32	gibberella	946	112.5	3.2	614	2	Q8VND4_LACDL	Q8VND4	lacdl
874	115	3.3	1895	2	Q3ORL3_9RHOB	Q3ORL3	silicibacte	947	112.5	3.2	638	1	SRPR_CANPA	SRPR	canpa
875	115	3.3	3966	1	RPOA_PRR81	RPOA	p replicase	948	112.5	3.2	815	2	Q8N5C4_HUMAN	Q8N5C4	human
876	114.5	3.3	408	2	Q29129_TDRBR	Q29129	tadarida br	949	112.5	3.2	858	2	Q55N21_CRYNE	Q55N21	cryne
877	114.5	3.3	586	2	Q5GQW7_9CAUD	Q5GQW7	bacteriopho	950	112.5	3.2	858	2	Q5K3F0_CRYNE	Q5K3F0	cryne
878	114.5	3.3	620	2	Q7NWM1_CHRYO	Q7NWM1	chromobacte	951	112.5	3.2	909	2	Q6MP91_BDEBA	Q6MP91	bdeba
879	114.5	3.3	806	1	SRPR_MOUSE	SRPR	mus musculu	952	112.5	3.2	1015	2	Q2V4T0_CAEEL	Q2V4T0	caeel
880	114.5	3.3	865	2	Q21PX2_9DELT	Q21PX2	anaeromyxob	953	112.5	3.2	1028	2	Q76836_CAEEL	Q76836	caeel
881	114.5	3.3	829	2	Q4N9H1_THERA	Q4N9H1	thellieria p	954	112.5	3.2	1075	1	TARSH_HUMAN	TARSH	human
882	114.5	3.3	915	2	Q5R8H9_PONPY	Q5R8H9	pongo pygma	955	112.5	3.2	1087	2	Q7Y400_9CAUD	Q7Y400	9caud
883	114.5	3.3	931	2	Q91995_XENLA	Q91995	xenopus lae	956	112.5	3.2	1204	2	Q3HHE8_TRIER	Q3HHE8	trier
884	114.5	3.3	1052	2	Q3GCK5_9FIRM	Q3GCK5	syntrophomo	957	112.5	3.2	1309	2	Q6CC11_YARLI	Q6CC11	yarli
885	114.5	3.3	1105	2	Q389F7_9TRYP	Q389F7	trypanosoma	958	112.5	3.2	1909	2	Q91RX3_ARATH	Q91RX3	arath
886	114.5	3.3	1378	2	Q5L6J2_CHLAB	Q5L6J2	chlamydomo	959	112.5	3.2	1984	2	Q90BH5_9RHAB	Q90BH5	9rhab
887	114.5	3.3	1542	2	Q5BCK3_EMENT	Q5BCK3	aspergillus	960	112.5	3.2	2186	2	Q5HPI8_STAAC	Q5HPI8	staac
888	114.5	3.3	1756	2	Q751S9_ORYSA	Q751S9	oryza sativ	961	112	3.2	152	2	Q8WVP6_9ASCI	Q8WVP6	9asci
889	114.5	3.3	16311	2	Q3AR72_CHLCH	Q3AR72	chlorobium	962	112	3.2	231	2	Q8N882_HUMAN	Q8N882	human
890	114	3.3	200	2	Q9Y4S8_HUMAN	Q9Y4S8	homo sapien	963	112	3.2	389	2	Q5ASR4_EMENT	Q5ASR4	ement
891	114	3.3	227	2	Q6FHW5_HUMAN	Q6FHW5	homo sapien	964	112	3.2	400	2	Q3W769_9ACRO	Q3W769	9acro
892	114	3.3	227	2	Q71CA7_HUMAN	Q71CA7	homo sapien	965	112	3.2	484	2	Q91OW1_PSEAE	Q91OW1	pseae
893	114	3.3	237	2	Q3MMW9_9DELT	Q3MMW9	syntrophoba	966	112	3.2	553	2	Q30UL3_THIDN	Q30UL3	thidn
894	114	3.3	563	2	Q9UTU6_TGEBI	Q9UTU6	zygosaacchar	967	112	3.2	555	2	Q906R7_DERPA	Q906R7	derpa
895	114	3.3	580	2	Q5VQ66_ORYSA	Q5VQ66	oryza sativ	968	112	3.2	567	2	Q9C9Y9_ARATH	Q9C9Y9	arath
896	114	3.3	597	1	NF2L2_MOUSE	NF2L2	mus musculu	969	112	3.2	575	2	Q74B80_GEOSL	Q74B80	geosl
897	114	3.3	628	2	Q3UOKO_MOUSE	Q3UOKO	mus musculu	970	112	3.2	618	2	Q4RH76_TETNG	Q4RH76	tetng
898	114	3.3	628	2	Q4S3J7_TETNG	Q4S3J7	tetradodon n	971	112	3.2	674	2	Q6PMR3_GVIRU	Q6PMR3	gviru
899	114	3.3	687	2	Q3E273_CHLAD	Q3E273	chloroflexu	972	112	3.2	710	2	Q32914_MYCLE	Q32914	mycle
900	114	3.3	702	2	Q2U444_ASPOR	Q2U444	aspergillus	973	112	3.2	733	2	Q9CB88_MYCLE	Q9CB88	mycle
901	114	3.3	786	2	Q9RZL4_DEIRA	Q9RZL4	deinococcus	974	112	3.2	756	2	Q44YX0_9BURK	Q44YX0	9burk
902	114	3.3	794	2	Q18742_BOVIN	Q18742	bos taurus	975	112	3.2	761	2	Q6MG74_RAT	Q6MG74	rat
903	114	3.3	805	2	Q2QX81_ORYSA	Q2QX81	oryza sativ	976	112	3.2	881	2	Q8GMF9_STRGL	Q8GMF9	strgl
904	114	3.3	820	2	Q18743_BOVIN	Q18743	bos taurus	977	112	3.2	884	2	Q2Q2UP9_ORYSA	Q2Q2UP9	orysa
905	114	3.3	905	2	Q18741_BOVIN	Q18741	bos taurus	978	112	3.2	925	2	Q22ZP9_STRSU	Q22ZP9	strsu
906	114	3.3	1053	2	Q2QNP3_ORYSA	Q2QNP3	oryza sativ	979	112	3.2	1034	2	Q613E9_CAEER	Q613E9	caeer
907	114	3.3	1053	2	Q94143_ORYSA	Q94143	oryza sativ	980	112	3.2	1053	2	Q7XL61_ORYSA	Q7XL61	orysa

981	112	3.2	1174	2	Q7QC8_ANOGA	Q7qce8 anopheles g	1054	110.5	3.2	1456	1	RDRP_PVX	P0935 potato viru
982	112	3.2	1530	2	Q4P4C4_USTWA	Q4p4c4 ustilago ma	1055	110.5	3.2	1491	2	Q2KAF9_RHIET	Q2ka19 rhizobium e
983	112	3.2	1557	2	Q06652_DROME	Q06652 diosophila	1056	110.5	3.2	2166	2	Q068H1_STPAS	Q068h1 staphylococ
984	112	3.2	1617	2	Q8IKS0_PLAF7	Q8iks0 plasmidom	1057	110.5	3.2	2747	2	Q91800_AERSA	Q91800 aeromonas s
985	112	3.2	1660	2	Q0SIR1_ARATH	Q0sir1 arabidopsis	1058	110.5	3.2	2771	2	Q4UGJ7_THEAN	Q4ugj7 thelleria a
986	112	3.2	1660	2	Q4QERO_LEIMA	Q4qero leishmania	1059	110	3.1	352	1	D0F18_ARATH	Q04358 arabidopsis
987	112	3.2	2214	2	Q20219_CABEL	Q20219 caenorhabdi	1060	110	3.1	457	2	Q4RPO3_TETNG	Q4rp03 tetraodon n
988	112	3.2	2503	2	Q4TWM1_PRRSV	Q4twm1 porcine rep	1061	110	3.1	485	2	Q5NXX3_AZOSE	Q5nxx3 azorocid sp
989	112	3.2	2620	2	Q3NUK2_SHEPR	Q3nuk2 shewanella	1062	110	3.1	513	2	Q47B10_DECAR	Q47b10 dechloromon
990	112	3.2	3399	2	Q6LRT5_PHOPE	Q6lrt5 photobacter	1063	110	3.1	562	2	Q67B08_GINPA	Q67b08 giardia a
991	112	3.2	3960	2	Q0DLN8_PRRSV	Q0dlm8 porcine rep	1064	110	3.1	672	2	Q91VZ8_VIVRU	Q91vz8 hepatitis e
992	112	3.2	3960	2	Q9DLP0_PRRSV	Q9dlp0 porcine rep	1065	110	3.1	741	2	Q9PJU2_SCHPO	Q9pju2 schistosom
993	112	3.2	3960	2	Q9DLP1_PRRSV	Q9dlp1 porcine rep	1066	110	3.1	786	2	Q4UCG9_THEAN	Q4ucg9 thelleria a
994	112	3.2	4333	2	Q36YD8_RHOPE	Q36y8 rhodopseudo	1067	110	3.1	792	2	Q2RUM5_RHOBU	Q2rum5 rhodospirill
995	111.5	3.2	382	2	Q03990_DAUCA	Q03990 daucus caro	1068	110	3.1	821	2	Q4K9E7_PSEPS	Q4k9e7 pseudomonas
996	111.5	3.2	552	2	Q4N6B9_THEPA	Q4n6b9 thelleria p	1069	110	3.1	827	2	Q5FR97_GLUOX	Q5fr97 gluconobact
997	111.5	3.2	569	2	Q5EF57_9BURK	Q5ef57 acidovorax	1070	110	3.1	846	2	Q4PAA5_USTWA	Q4paa5 ustilago ma
998	111.5	3.2	691	2	Q5EF57_9BURK	Q5ef57 acidovorax	1071	110	3.1	853	2	Q7S3C5_NEUCR	Q7s3c5 neuropept
999	111.5	3.2	699	2	Q3CIY4_PALPH	Q3ciy4 mycoplasma	1072	110	3.1	853	2	Q8VUZ6_ANNAP	Q8vuz6 anabaena sp
1000	111.5	3.2	798	2	Q9U225_CAEEL	Q9u225 chlamydiae	1073	110	3.1	853	2	Q5JUD5_ORYSA	Q5jud5 oryza sativ
1001	111.5	3.2	825	2	Q873Y0_ASPPU	Q873y0 aspergillus	1074	110	3.1	901	2	Q59PF9_CANAL	Q59pf9 candida alb
1002	111.5	3.2	894	2	Q51FW4_ENTHI	Q51fw4 entamoeba h	1075	110	3.1	908	2	Q55Y53_CRYNE	Q55y53 cryptococcu
1003	111.5	3.2	989	2	Q94909_HUMAN	Q94909 homo sapien	1076	110	3.1	916	2	Q51UQ7_ORYSA	Q51uq7 oryza sativ
1004	111.5	3.2	1133	2	Q7SCS8_NEUCR	Q7scs8 neuropept	1077	110	3.1	932	2	Q5AXT3_EMENT	Q5axt3 aspergillus
1005	111.5	3.2	1202	2	Q8MY43_PPTST	Q8my43 eptactretus	1078	110	3.1	940	2	Q2LZ00_DROPS	Q2lzo0 drosoophila
1006	111.5	3.2	1320	2	Q4PEU9_USTWA	Q4pe9 ustilago ma	1079	110	3.1	1006	2	Q5SRK6_CRYNE	Q5srk6 cryptococcu
1007	111.5	3.2	1456	2	Q2UGJ4_ASPPOR	Q2ugj4 aspergillus	1080	110	3.1	1006	2	Q5KRF02_CRYNE	Q5krf02 cryptococcu
1008	111.5	3.2	1456	2	Q4H4H8_PVX	Q4h4h8 potaro viru	1081	110	3.1	1009	2	Q55R69_CRYNE	Q55r69 cryptococcu
1009	111.5	3.2	1678	2	Q3UGI8_MOUSE	Q3ugi8 mus musculu	1082	110	3.1	1009	2	Q5KRF01_CRYNE	Q5krf01 cryptococcu
1010	111.5	3.2	1742	2	Q7TTP1_MOUSE	Q7t1 mus musculu	1083	110	3.1	1027	2	Q37LP3_RHOPE	Q37lp3 rhodopseudo
1011	111.5	3.2	1984	2	Q9QBH1_PRRAB	Q9qbh1 viral hemor	1084	110	3.1	1057	2	Q4P5X6_USTWA	Q4p5x6 ustilago ma
1012	111.5	3.2	1984	2	Q9QV4_9RHAB	Q9qv4 viral hemor	1085	110	3.1	1073	2	Q6C0R9_YARLT	Q6c0r9 yarrowia ll
1013	111.5	3.2	1984	2	Q9QV0_9RHAB	Q9qv0 viral hemor	1086	110	3.1	1094	2	Q7RX91_NEUCR	Q7rx91 neuropept
1014	111.5	3.2	8173	2	Q7UD8_RHOBA	Q7ud8 rhodopirell	1087	110	3.1	1110	2	Q5P47_CRYNE	Q5p47 cryptococcu
1015	111	3.2	327	2	Q2MM20_STRTT	Q2mm20 streptococc	1088	110	3.1	1110	2	Q5KEA9_CRYNE	Q5kea9 cryptococcu
1016	111	3.2	332	2	Q4KCT1_PSEPS	Q4kct1 pseudomonas	1089	110	3.1	1148	2	Q7TS92_MOUSE	Q7ts92 mus musculu
1017	111	3.2	342	2	Q54VY1_PICDI	Q54v1 dictyosteli	1090	110	3.1	1155	2	Q3UHP2_MOUSE	Q3uhp2 mus musculu
1018	111	3.2	381	2	Q6Z5E1_CAEER	Q6z5e1 caenorhabdi	1091	110	3.1	1160	2	Q924U7_MOUSE	Q924u7 mus musculu
1019	111	3.2	445	2	Q89F39_BRAB	Q89f39 bradyrhizob	1092	110	3.1	1205	2	Q9LAT9_ANNAP	Q9lat9 anabaena p
1020	111	3.2	531	2	Q365I3_9GAMA	Q365i3 shewanella	1093	110	3.1	1205	2	Q9RPM8_ANNAP	Q9rpm8 anabaena p
1021	111	3.2	562	2	Q67120_GINPA	Q67120 influenza a	1094	110	3.1	1351	2	Q31V22_SHIBS	Q31v22 shigella bo
1022	111	3.2	582	2	Q7NSP1_CHRVO	Q7nsf1 chromobacte	1095	110	3.1	1367	1	MUC1_YEAST	Q06840 saccharomyc
1023	111	3.2	598	2	Q3IEN8_THICR	Q3ien8 thiomicrosp	1096	110	3.1	1367	2	Q6LCS8_SACDI	Q6lcs8 saccharomyc
1024	111	3.2	757	2	Q3IKS_THICR	Q3iks thiomicrosp	1097	110	3.1	1456	2	Q91KX2_PVX	Q91kx2 potato viru
1025	111	3.2	850	2	Q3N2X5_9DELTA	Q3n2x5 syntrophoba	1098	110	3.1	1731	2	Q4Q981_LEIMA	Q4q981 leishmania
1026	111	3.2	860	2	Q4R84_TETNG	Q4r84 tetraodon n	1099	110	3.1	1966	2	Q4WU47_ASPPU	Q4wu47 aspergillus
1027	111	3.2	924	2	Q5KLT6_CRYNE	Q5klt6 cryptococcu	1100	109.5	3.1	384	2	Q8GVG6_ORYSA	Q8gv6 oryza sativ
1028	111	3.2	1002	2	Q8GZY5_ORYSA	Q8gzy5 oryza sativ	1101	109.5	3.1	387	2	Q4D265_TRYCR	Q4d265 trypanosoma
1029	111	3.2	1004	2	Q8PU63_METMA	Q8pu63 methanosaic	1102	109.5	3.1	560	2	Q91P65_MYCSY	Q91p65 mycoplasma
1030	111	3.2	1053	2	Q2R4K7_ORYSA	Q2r4k7 oryza sativ	1103	109.5	3.1	622	2	Q7SR50_NEUCR	Q7sr50 neuropept
1031	111	3.2	1085	2	Q3D9W7_STRAG	Q3d9w7 streptococc	1104	109.5	3.1	633	2	Q4MW71_ASPPU	Q4mw71 aspergillus
1032	111	3.2	1115	2	Q3S2Y8_STRAG	Q3s2y8 streptococc	1105	109.5	3.1	638	2	Q5RAC7_PONPY	Q5rac7 pongo pygma
1033	111	3.2	1189	2	Q5CTAO_CRYPV	Q5cto cryptospori	1106	109.5	3.1	644	2	Q41B25_GIBZE	Q41b25 gibberella
1034	111	3.2	1194	2	Q6BYH4_DEBNA	Q6byh4 debaryomyce	1107	109.5	3.1	667	1	K0431_HUMAN	Q043084 homo sapien
1035	111	3.2	1205	2	Q49BA6_STRAG	Q49ba6 streptococc	1108	109.5	3.1	779	2	Q4H084_FREDI	Q4h084 firemyella d
1036	111	3.2	1222	2	Q8MY44_EPTST	Q8my44 eptactretus	1109	109.5	3.1	862	2	Q3PRR4_NITHA	Q3pr4 nitroabacter
1037	111	3.2	1239	2	Q7X5P9_ANNAP	Q7x5p9 anabaena p	1110	109.5	3.1	877	2	Q4Y3Z3_PLACH	Q4y3z3 plantamodum
1038	111	3.2	1241	2	Q8LLO4_ARATH	Q8lll4 arabidopsis	1111	109.5	3.1	1077	2	Q448G5_SOLUS	Q448g5 solibacter
1039	111	3.2	1578	2	Q57YR3_9TRYP	Q57yr3 trypanosoma	1112	109.5	3.1	1151	2	Q55L95_CRYNE	Q55l95 cryptococcu
1040	111	3.2	2037	2	Q9PVZ2_XENLA	Q9pvz2 xenopus lae	1113	109.5	3.1	1151	2	Q5KAB9_CRYNE	Q5kab9 cryptococcu
1041	111	3.2	2503	2	Q9ENK6_PRRSV	Q9enk6 porcine rep	1114	109.5	3.1	1459	2	Q3KW17_GRHIZ	Q3kw17 mesorhizobi
1042	111	3.2	3960	1	RPOA_PRRSV	Q9wj2 p replicase	1115	109.5	3.1	1809	1	TSC2_RAT	Q9816 ratcus nov
1043	110.5	3.2	409	2	Q8IR01_DROME	Q8ir01 diosophila	1116	109.5	3.1	1984	2	Q9WME7_9RHAB	Q9wme7 viral hemor
1044	110.5	3.2	504	2	Q6J4Y8_CHICK	Q6j4y8 gallus gall	1117	109.5	3.1	3181	2	Q6MKN7_PARRU	Q6mkn7 parichlamyd
1045	110.5	3.2	695	2	Q2U6F7_ASPPOR	Q2u6f7 aspergillus	1118	109.5	3.1	4408	2	Q44AC0_SOLUS	Q44ac0 solibacter
1046	110.5	3.2	779	2	Q50588_PSEHY	Q50588 pseudomonas	1119	109.5	3.1	4920	2	Q4KKE3_PSEPS	Q4kke3 pseudomonas
1047	110.5	3.2	885	2	Q8MW6_HUMAN	Q8mw6 homo sapien	1120	109.5	3.1	7342	2	Q3XG91_9PROT	Q3xg91 magnetococ
1048	110.5	3.2	885	2	Q5SKS5_CRYNE	Q5sks5 cryptococcu	1121	109	3.1	270	2	Q9A3H3_CAUCR	Q9a3h3 caulobacter
1049	110.5	3.2	885	2	Q5KAQ0_CRYNE	Q5kaq0 cryptococcu	1122	109	3.1	302	2	Q43UAD2_SOLUS	Q43uad2 solibacter
1050	110.5	3.2	1040	1	IF2_BACTN	Q8a2a1 bacteroides	1123	109	3.1	452	2	Q9SC06_ARATH	Q9sc06 arabidopsis
1051	110.5	3.2	1066	1	Q22804_ARATH	Q22804 arabidopsis	1124	109	3.1	489	1	ANTR2_HUMAN	P58335 homo sapien
1052	110.5	3.2	1081	1	MED15_YEAST	P19669 s rna polym	1125	109	3.1	496	2	Q6ZTG1_HUMAN	Q6ztg1 homo sapien
1053	110.5	3.2	1176	2	Q3AZB7_SYNS9	Q3azb7 synechococc	1126	109	3.1	795	2	Q96PV6_HUMAN	Q96pv6 homo sapien

1127	109	3.1	802	2	Q19764_CAEEL	Q19764 caenorhabdi	1200	108	3.1	538	2	Q6SPF0_HUMAN	Q6SPF0 homo sapien
1128	109	3.1	851	2	Q9VH91_DROME	Q9VH91 drosophila	1201	108	3.1	562	2	Q4ZH98_GINPA	Q4ZH98 influenza a
1129	109	3.1	806	2	Q4HQ23_CAMUP	Q4HQ23 campylobact	1202	108	3.1	562	2	Q67123_GINPA	Q67123 influenza a
1130	109	3.1	927	2	Q93G12_MORBO	Q93G12 moraxella b	1203	108	3.1	572	2	Q2Y920_NITMU	Q2Y920 nitratospir
1131	109	3.1	985	2	Q94J41_ORYSA	Q94J41 oryza sativ	1204	108	3.1	581	2	Q4Q203_LEIMA	Q4Q203 leishmania
1132	109	3.1	987	2	Q65WK6_ORYSA	Q65WK6 oryza sativ	1205	108	3.1	623	2	Q4INF3_METBU	Q4INF3 methanococ
1133	109	3.1	1053	2	Q60F03_ORYSA	Q60F03 oryza sativ	1206	108	3.1	635	2	Q612N5_CAEAR	Q612N5 caenorhabdi
1134	109	3.1	1053	2	Q65V31_ORYSA	Q65V31 oryza sativ	1207	108	3.1	645	2	Q9H048_HUMAN	Q9H048 homo sapien
1135	109	3.1	1091	2	Q06556_STRDY	Q06556 streptococc	1208	108	3.1	660	2	Q9YLK2_VIRU	Q9YLK2 hepatitis e
1136	109	3.1	1102	2	Q872D9_NEUCR	Q872D9 neurospora	1209	108	3.1	674	2	Q6BD83_VIRU	Q6BD83 hepatitis e
1137	109	3.1	1159	2	Q3PRW7_NITHA	Q3PRW7 nitrobacter	1210	108	3.1	674	2	Q7TGP1_VIRU	Q7TGP1 hepatitis e
1138	109	3.1	1182	2	Q24552_DROME	Q24552 drosophila	1211	108	3.1	674	2	Q8JUN2_VIRU	Q8JUN2 hepatitis e
1139	109	3.1	1182	2	Q9VCS3_DROME	Q9VCS3 drosophila	1212	108	3.1	675	2	Q4WP66_ASPFU	Q4WP66 aspergillus
1140	109	3.1	1187	2	Q8MY42_EPTST	Q8MY42 eptretetus	1213	108	3.1	706	2	Q47M06_THERY	Q47M06 thermobifid
1141	109	3.1	1242	2	Q9W05_DROME	Q9W05 drosophila	1214	108	3.1	757	1	TAU_HUMAN	TAU homo sapien
1142	109	3.1	1253	2	Q7XT19_ORYSA	Q7XT19 oryza sativ	1215	108	3.1	759	2	Q2UGV8_ASPOR	Q2UGV8 aspergillus
1143	109	3.1	1425	2	Q86CW3_DROSE	Q86CW3 drosophila	1216	108	3.1	768	2	Q9VH92_DROME	Q9VH92 hepatitis e
1144	109	3.1	1602	2	Q4PCU7_USTMA	Q4PCU7 ustilago ma	1217	108	3.1	777	2	Q311J7_THICK	Q311J7 thiomicrosp
1145	109	3.1	1614	2	Q69Y09_HUMAN	Q69Y09 homo sapien	1218	108	3.1	784	2	Q8INN6_DROME	Q8INN6 drosophila
1146	109	3.1	1739	2	Q4W2V7_PLARE	Q4W2V7 plasmodium	1219	108	3.1	803	2	Q6A065_MOUSE	Q6A065 mus musculu
1147	109	3.1	1756	2	Q3UGK8_DROME	Q3UGK8 drosophila	1220	108	3.1	823	2	Q39ES1_BUR83	Q39ES1 burkholderi
1148	109	3.1	1785	2	Q3UGK8_MOUSE	Q3UGK8 mus musculu	1221	108	3.1	836	2	Q7XYX2_ARATH	Q7XYX2 arabidopsis
1149	109	3.1	1872	2	Q6FYV5_BAROU	Q6FYV5 bartonella	1222	108	3.1	906	2	Q54WV3_DICDI	Q54WV3 dictyosteli
1150	109	3.1	1928	2	Q4PBO6_USTMA	Q4PBO6 ustilago ma	1223	108	3.1	931	2	Q7S500_NEUCR	Q7S500 neurospora
1151	109	3.1	5017	2	Q81FJ0_BACCR	Q81FJ0 bacillus ce	1224	108	3.1	998	2	Q12869_HUMAN	Q12869 homo sapien
1152	108.5	3.1	300	2	Q3SE19_9BRAD	Q3SE19 bradyrhizob	1225	108	3.1	1053	2	Q5VM23_ORYSA	Q5VM23 oryza sativ
1153	108.5	3.1	421	2	Q4QV5_PLABE	Q4QV5 plasmodium	1226	108	3.1	1156	2	Q2K210_RHIEF	Q2K210 rhizobium e
1154	108.5	3.1	490	2	Q58315_9TRYP	Q58315 trypanosoma	1227	108	3.1	1231	2	Q85170_ANAPH	Q85170 anaplasmu p
1155	108.5	3.1	490	2	Q968P6_PLAVI	Q968P6 plasmodium	1228	108	3.1	1231	2	Q7BS53_ANAPH	Q7BS53 anaplasmu p
1156	108.5	3.1	606	2	P90573_PLABE	P90573 plasmodium	1229	108	3.1	1231	2	Q9JRL4_9RICK	Q9JRL4 entrichia s
1157	108.5	3.1	629	2	Q4USY6_XANCP	Q4USY6 xanthomonas	1230	108	3.1	1231	2	Q9JUR03_ANAPH	Q9JUR03 anaplasmu p
1158	108.5	3.1	639	2	Q8PAN0_XANCP	Q8PAN0 xanthomonas	1231	108	3.1	1242	2	Q6N306_RHOPA	Q6N306 rhodospo
1159	108.5	3.1	652	1	Q3MHB8_BOVIN	Q3MHB8 bos taurus	1232	108	3.1	1262	2	Q35XJ2_9GAMW	Q35XJ2 shewanella
1160	108.5	3.1	652	1	UHP2_SCHPO	UHP2 scyphosacch	1233	108	3.1	1268	1	SC24B_HUMAN	SC24B homo sapien
1161	108.5	3.1	660	2	Q514T2_VIRU	Q514T2 hepatitis e	1234	108	3.1	1299	2	Q6P4R8_HUMAN	Q6P4R8 homo sapien
1162	108.5	3.1	660	2	Q514T5_VIRU	Q514T5 hepatitis e	1235	108	3.1	1344	2	Q15312_HUMAN	Q15312 homo sapien
1163	108.5	3.1	678	2	Q2QR67_ORYSA	Q2QR67 oryza sativ	1236	108	3.1	1520	2	Q4PBP6_USTMA	Q4PBP6 ustilago ma
1164	108.5	3.1	681	2	Q9FFW5_ARATH	Q9FFW5 arabidopsis	1237	108	3.1	1556	2	Q91BE1_FUGRU	Q91BE1 fugu rubrip
1165	108.5	3.1	682	2	Q3TY26_MOUSE	Q3TY26 m viralis co	1238	108	3.1	1634	2	Q9XW25_CAEEL	Q9XW25 caenorhabdi
1166	108.5	3.1	682	2	Q3ULB5_MOUSE	Q3ULB5 mus musculu	1239	108	3.1	1640	2	Q3F3K8_9BURK	Q3F3K8 burkholderi
1167	108.5	3.1	724	2	Q9H6S7_HUMAN	Q9H6S7 homo sapien	1240	108	3.1	1698	2	Q5SWE2_CRYNE	Q5SWE2 cryptococcu
1168	108.5	3.1	738	2	Q5B3B1_EMENT	Q5B3B1 aspergillus	1241	108	3.1	1870	2	Q7SDE6_NEUCR	Q7SDE6 neurospora
1169	108.5	3.1	784	2	Q5BER8_BKARE	Q5BER8 brachydanio	1242	108	3.1	1977	2	Q83TF5_STRCZ	Q83TF5 streptomyce
1170	108.5	3.1	860	2	Q6J614_ENTCL	Q6J614 entrobacte	1243	108	3.1	2728	2	Q583J1_9TRYP	Q583J1 trypanosoma
1171	108.5	3.1	866	2	Q5KEA7_CRYNE	Q5KEA7 cryptococcu	1244	108	3.1	4007	2	Q7SHZ4_NEUCR	Q7SHZ4 neurospora
1172	108.5	3.1	877	2	Q6DMK4_ENTCL	Q6DMK4 entrobacte	1245	108	3.1	10495	2	Q4R9E2_TETNG	Q4R9E2 tetraodon n
1173	108.5	3.1	881	2	Q2KI05_BORAV	Q2KI05 bordetella	1246	107.5	3.1	172	2	Q5GN53_MYOCO	Q5GN53 myocastor c
1174	108.5	3.1	954	2	Q3FCF7_DBURK	Q3FCF7 burkholderi	1247	107.5	3.1	201	2	Q4XHC4_PLACH	Q4XHC4 plach
1175	108.5	3.1	971	2	Q6W3C4_CAEEL	Q6W3C4 caenorhabdi	1248	107.5	3.1	253	2	Q8MUV6_SCHHA	Q8MUV6 schistosoma
1176	108.5	3.1	989	2	Q19930_CAEEL	Q19930 caenorhabdi	1249	107.5	3.1	355	2	Q7W152_BORPA	Q7W152 borpha
1177	108.5	3.1	995	2	Q69V30_ORYSA	Q69V30 oryza sativ	1250	107.5	3.1	363	2	Q31JH9_THICK	Q31JH9 thiomicrosp
1178	108.5	3.1	1188	2	Q7PPI1_ANOGA	Q7PPI1 anopheles g	1251	107.5	3.1	386	2	Q4CZ98_TRYCR	Q4CZ98 trypanosoma
1179	108.5	3.1	1209	1	TRIF6_MOUSE	TRIF6 mus musculu	1252	107.5	3.1	509	2	Q8ZC12_YERPE	Q8ZC12 yerstania pe
1180	108.5	3.1	1376	2	Q7SSH8_NEUCR	Q7SSH8 neurospora	1253	107.5	3.1	513	2	Q3XS77_9PROT	Q3XS77 magnetococc
1181	108.5	3.1	1409	1	RPOC_RALSO	RPOC talistonia s	1254	107.5	3.1	539	2	Q3W8S0_9ACTO	Q3W8S0 frantia sp.
1182	108.5	3.1	1513	2	Q5KNH8_CRYNE	Q5KNH8 cryptococcu	1255	107.5	3.1	636	2	Q3KRC3_RAT	Q3KRC3 rattus norv
1183	108.5	3.1	1623	2	Q4RK63_TETNG	Q4RK63 tetraodon n	1256	107.5	3.1	647	1	SF04_RAT	SF04 rattus norv
1184	108.5	3.1	1689	2	Q8QZF4_VIRU	Q8QZF4 cricmean-con	1257	107.5	3.1	667	2	Q6BNC9_HUMAN	Q6BNC9 homo sapien
1185	108.5	3.1	1689	2	Q991H9_VIRU	Q991H9 cricmean-con	1258	107.5	3.1	674	2	Q5B9S6_EMENT	Q5B9S6 aspergillus
1186	108.5	3.1	1779	2	Q52374_PFRIM	Q52374 caldicellula g	1259	107.5	3.1	792	2	Q6FYB5_CANGA	Q6FYB5 candida gla
1187	108.5	3.1	1826	2	Q7Q6K9_ANOGA	Q7Q6K9 anopheles g	1260	107.5	3.1	810	2	Q7ULV8_RHOBA	Q7ULV8 rhodopirell
1188	108.5	3.1	1845	2	Q3NZ54_9GAMW	Q3NZ54 shewanella	1261	107.5	3.1	833	2	Q5B418_EMENT	Q5B418 aspergillus
1189	108.5	3.1	2732	2	Q9J3F2_9CORO	Q9J3F2 murine hepa	1262	107.5	3.1	940	2	Q7XTN8_ORYSA	Q7XTN8 oryza sativ
1190	108.5	3.1	2733	2	Q7NN3_9CORO	Q7NN3 murine hepa	1263	107.5	3.1	954	2	Q59PV2_CANAL	Q59PV2 candida alb
1191	108.5	3.1	3269	2	Q9RGN5_LACRE	Q9RGN5 lactobacill	1264	107.5	3.1	964	2	Q3BPK5_9TRYP	Q3BPK5 trypanosoma
1192	108.5	3.1	7124	1	RIAB_CTM2	RIAB repiliase	1265	107.5	3.1	977	2	Q6K319_ORYSA	Q6K319 oryza sativ
1193	108	3.1	242	2	Q3PQH3_NITHA	Q3PQH3 nitrobacter	1266	107.5	3.1	1051	2	Q43WV4_SOLUS	Q43WV4 solibacter
1194	108	3.1	316	2	Q6CVZ2_YARLI	Q6CVZ2 yarrowia li	1267	107.5	3.1	1170	1	SCAR4_ARATH	SCAR4 arabidopsis
1195	108	3.1	417	2	Q84NK6_ORYSA	Q84NK6 oryza sativ	1268	107.5	3.1	1208	2	Q4PEL0_USTMA	Q4PEL0 ustilago ma
1196	108	3.1	480	2	Q66T11_XENLA	Q66T11 xenopus lae	1269	107.5	3.1	1249	2	Q59XK7_CANAL	Q59XK7 candida alb
1197	108	3.1	511	1	EGRI_BRARE	EGRI brachydanio	1270	107.5	3.1	1256	2	Q6D975_ERWCT	Q6D975 erwina car
1198	108	3.1	512	2	Q4ZYG5_PSEU2	Q4ZYG5 pseudomonas	1271	107.5	3.1	1260	2	Q2UBW2_ASPOR	Q2UBW2 aspergillus
1199	108	3.1	537	2	Q4INS5_GIBZE	Q4INS5 gibberella	1272	107.5	3.1	1501	2	Q9SD86_ARATH	Q9SD86 arabidopsis



1273	107.5	3.1	1604	2	055JP5_CRYNE	055JP5_cryptococcu	1346	106.5	3.0	794	1	PMS1_SCHPO	P54280_schizosach
1274	107.5	3.1	1689	2	08QZF5_VIRU	08qzf5 crimanen-con	1347	106.5	3.0	800	1	KIN4_YEAST	001919 saccharomyc
1275	107.5	3.1	1747	2	05PA51_ANAMU	05pa51 aniplasma m	1348	106.5	3.0	841	2	084TM6_HELPY	084TM6_helicobacte
1276	107.5	3.1	1899	2	0303R2_STRSU	0303r2 streptococc	1349	106.5	3.0	931	2	091655_BACPI	091655 bacillus f1
1277	107.5	3.1	2112	2	09VEI9_DROME	09vei9 dirosophila	1350	106.5	3.0	966	2	07PNK8_ANOGA	07pnk8 anopheles g
1278	107.5	3.1	2642	2	02ZRR9_SHEPU	02zrr9 shewanelia	1351	106.5	3.0	1047	2	074BT1_GEOSL	074bt1 geobacter s
1279	107.5	3.1	2644	2	02X787_9GAMM	02x787 shewanelia	1352	106.5	3.0	1058	2	0851R2_ORYSA	0851r2 oryza sativ
1280	107	3.1	363	1	LYPD3_MOUSE	091ykr8 mus musculu	1353	106.5	3.0	1161	2	09EP53_MOUSE	09ep53 mus musculu
1281	107	3.1	371	2	03RU03_RALME	03ru03 ralsconia m	1354	106.5	3.0	1269	2	03PS26_NITRA	03ps26 nitrobacter
1282	107	3.1	404	2	06W222_RHISM	06w222 rhizobium s	1355	106.5	3.0	1332	2	08MSX3_DROME	08msx3 dirosophila
1283	107	3.1	432	2	059197_BACCI	059197 bacillus ci	1356	106.5	3.0	1343	2	06CX23_YARLI	06cx23 yarrowia l1
1284	107	3.1	513	2	08G5K3_EIFLU	08g5k3 blifidobacte	1357	106.5	3.0	1382	2	05KRK2_CRYNE	05krk2 cryptococcu
1285	107	3.1	550	2	06SPE9_RABIT	06spe9 crytocolagus	1358	106.5	3.0	1431	2	03ME76_ANAVT	03me76 anabaena va
1286	107	3.1	562	2	067333_IASIN	067333 influenza a	1359	106.5	3.0	1501	2	02UKS5_ASPPR	02uks5 aspergillus
1287	107	3.1	612	2	08CIDI_MOUSE	08cidi mus musculu	1360	106.5	3.0	1543	2	07K566_DROME	07k566 dirosophila
1288	107	3.1	616	2	06KZZ0_PICTO	06kzz0 picophilus	1361	106.5	3.0	1578	2	09BMW9_HUMAN	09bmw9 homo sapien
1289	107	3.1	616	2	099K31_MOUSE	099k31 mus musculu	1362	106.5	3.0	1658	2	03LHL9_DROME	03lhl9 dirosophila
1290	107	3.1	674	2	06BD78_VIRU	06bd78 hepaticis e	1363	106.5	3.0	1728	2	03PWE1_NITRA	03pwe1 nitrobacter
1291	107	3.1	683	2	04SBR2_TETNG	04sbr2 tetraodon n	1364	106.5	3.0	1761	2	07LBC6_HUMAN	07lbc6 homo sapien
1292	107	3.1	704	2	04MM72_ASPPU	04mm72 aspergillus	1365	106.5	3.0	1787	2	09UPS0_HUMAN	09ups0 homo sapien
1293	107	3.1	774	2	05SLQ1_CRYNE	05slq1 cryptococcu	1366	106.5	3.0	2139	2	04PDM0_USTWA	04pdm0 ustillaq ma
1294	107	3.1	774	2	05K922_CRYNE	05k922 cryptococcu	1367	106.5	3.0	2727	2	06NR00_DROME	06nr00 dirosophila
1295	107	3.1	774	2	05KDB7_CRYNE	05kdb7 cryptococcu	1368	106.5	3.0	2727	2	09VU06_DROME	09vu06 dirosophila
1296	107	3.1	789	2	06CS14_KLUUA	06cs14 kluyveromyc	1369	106.5	3.0	5094	2	021ZL4_RHOPA	021z14 rhodopseudo
1297	107	3.1	835	2	07UY68_RHOPA	07uy68 rhodopirell	1370	106	3.0	351	2	039492_CHLEU	039492 chlamydomon
1298	107	3.1	856	2	09SY11_ARATH	09sy11 arabidopsis	1371	106	3.0	456	2	02VYMO_MAGSA	02vymo magnetospir
1299	107	3.1	880	2	084WV4_ARATH	084wv4 arabidopsis	1372	106	3.0	480	2	04UQJ2_9GAMM	04uqj2 methyllobact
1300	107	3.1	880	2	094C84_ARATH	094c84 arabidopsis	1373	106	3.0	523	2	03SBR1_9BRAD	03sbr1 brachyrlabact
1301	107	3.1	930	2	040X22_KINRA	040x22 kinetococcus	1374	106	3.0	531	2	022367_9GAMM	022367 shewanelia
1302	107	3.1	944	2	07RY29_NEUCR	07ry29 neurospora	1375	106	3.0	550	2	08UTV3_VIRU	08utv3 hepatitis e
1303	107	3.1	964	2	05GX30_XANOR	05gx30 xanthomonas	1376	106	3.0	602	2	09SKR2_DROME	09skr2 dirosophila
1304	107	3.1	1053	2	05VMS2_ORYSA	05vms2 oryza sativ	1377	106	3.0	604	2	05KDO3_CRYNE	05kdo3 cryptococcu
1305	107	3.1	1070	2	02PI06_ASPPR	02pi06 aspergillus	1378	106	3.0	613	2	06ORF3_ORYSA	06orf3 oryza sativ
1306	107	3.1	1163	1	TSCI_RAT	092i16 aspergillus	1379	106	3.0	632	2	046UJ3_PROMT	046uj3 prochloroco
1307	107	3.1	1196	2	05H935_HUMAN	05h935 homo sapien	1380	106	3.0	636	2	08JTM4_LSDPY	08jtm4 lumby skin
1308	107	3.1	1200	2	05TPW6_ANOGA	05tpw6 anopheles g	1381	106	3.0	671	2	08JTM1_VIRU	08jtm1 hepatitis e
1309	107	3.1	1205	2	02W610_MAGSA	02w610 magnetospir	1382	106	3.0	674	2	08JUN6_VIRU	08jun6 hepatitis e
1310	107	3.1	1231	2	06CL75_KLUUA	06cl75 kluyveromyc	1383	106	3.0	680	2	0217P4_VIRU	0217p4 bacteriophila
1311	107	3.1	1245	2	03A968_CARHZ	03a968 carboxydoth	1384	106	3.0	691	2	09RZS7_DEIRA	09rzs7 diennococcus
1312	107	3.1	1264	2	07PDD1_PLAYO	07pdd1 plasmodium	1385	106	3.0	752	2	02UB42_ASPPR	02ub42 aspergillus
1313	107	3.1	1266	2	09VGL0_DROME	09vgl0 dirosophila	1386	106	3.0	785	2	054CE0_DICDI	054ce0 dicystostell
1314	107	3.1	1308	2	09DF77_CHICK	09df77 gallus gall	1387	106	3.0	830	2	059FN4_HUMAN	059fn4 homo sapien
1315	107	3.1	1350	2	02P7F6_XANOR	02p7f6 xanthomonas	1388	106	3.0	838	2	05AV13_EMENT	05av13 aspergillus
1316	107	3.1	1350	2	05H4M5_XANOR	05h4m5 xanthomonas	1389	106	3.0	839	1	IF2_HABDU	07v112 haemophilus
1317	107	3.1	1412	2	05SIX9_CRYNE	05slix9 cryptococcu	1390	106	3.0	857	2	06IRG8_RAT	06irg8 rattus norv
1318	107	3.1	1412	2	05KCS4_CRYNE	05kcs4 cryptococcu	1391	106	3.0	949	2	06ODS1_RAT	06ods1 rattus norv
1319	107	3.1	1450	2	09CE07_LACUA	09ce07 lactococcus	1392	106	3.0	963	2	09P759_NEUCR	09p759 neurospora
1320	107	3.1	1616	2	03YVW7_SHISS	03yv7 shigella so	1393	106	3.0	966	2	07XK78_ORYSA	07xk78 oryza sativ
1321	107	3.1	2887	2	03KGA0_PSEPP	03kga0 pseudomonas	1394	106	3.0	974	2	04WU27_ASPPU	04wu27 aspergillus
1322	107	3.1	2911	2	03JUS9_BURPI	03jus9 burkholderi	1395	106	3.0	996	2	08B3W1_PSSSM	08b3w1 pseudomonas
1323	107	3.1	2931	2	03EVR2_BACPI	03evr2 bacillus th	1396	106	3.0	1050	2	04PD88_USTWA	04pd88 ustillaq ma
1324	107	3.1	4540	2	07PS35_ANOGA	07ps35 anopheles g	1397	106	3.0	1060	2	07RYW5_NEUCR	07ryw5 neurospora
1325	107	3.1	5017	2	063DP3_BACCG	063df3 bacillus ce	1398	106	3.0	1072	1	MAP4_BOVIN	036225 bos taurus
1326	106.5	3.0	206	2	05SP07_BABRE	05spq7 brachydanio	1399	106	3.0	1085	2	06BD12_HUMAN	06bd12 homo sapien
1327	106.5	3.0	355	2	07WNU2_BORBR	07wnu2 bordetella	1400	106	3.0	1123	2	086106_DICDI	086106 d similari e
1328	106.5	3.0	358	2	04KD40_PSEFP	04kd40 pseudomonas	1401	106	3.0	1130	1	LATS1_HUMAN	095835 homo sapien
1329	106.5	3.0	363	2	03WB68_9ACTO	03wb68 frankia sp.	1402	106	3.0	1148	2	06MPH0_BDBBA	06mph0 bdellovibri
1330	106.5	3.0	363	2	03WH13_9ACTO	03wh13 frankia sp.	1403	106	3.0	1151	2	07S4R8_NEUCR	07s4r8 neurospora
1331	106.5	3.0	480	2	02LE02_9ACTO	02le02 streptomyc	1404	106	3.0	1235	2	06TEN8_BRARE	06ten8 brachydanio
1332	106.5	3.0	465	2	091W88_ARATH	091w88 arabidopsis	1405	106	3.0	1269	2	05V2A6_HALMA	05v2a6 halocaula
1333	106.5	3.0	490	2	03RT16_TALME	03rt16 ralsconia m	1406	106	3.0	1281	2	09V795_DROME	09v795 dirosophila
1334	106.5	3.0	503	2	07NUJ9_GLOVI	07nuj9 gloeobacter	1407	106	3.0	1335	2	04PIR5_USTWA	04pir5 ustillaq ma
1335	106.5	3.0	574	2	03V3A8_MOUSE	03v3a8 mus musculu	1408	106	3.0	1375	2	05SR47_CRYNE	05sr47 cryptococcu
1336	106.5	3.0	606	2	03GYU2_9ACTO	03gyu2 nocardioide	1409	106	3.0	1415	2	09HCF4_HUMAN	09hcf4 homo sapien
1337	106.5	3.0	638	1	SRPR_HUMAN	P08240 homo sapien	1410	106	3.0	1473	2	06UCV7_XANGG	06ucv7 xanthomonas
1338	106.5	3.0	660	2	02Z1X2_VIRU	02z1x2 hepatitis e	1411	106	3.0	1523	2	0813B1_PLA7	0813b1 plasmodium
1339	106.5	3.0	673	2	02UDG4_ASPPR	02udg4 aspergillus	1412	106	3.0	1534	2	09UID9_HUMAN	09uid9 homo sapien
1340	106.5	3.0	694	2	0541Q2_DICDI	0541q2 dicystostell	1413	106	3.0	1597	2	05IDE1_ENTHI	05ide1 entamoeba n
1341	106.5	3.0	703	2	061VP7_PHOPR	061vp7 phorbacter	1414	106	3.0	1699	2	05KJVE_CRYNE	05k1v6 cryptococcu
1342	106.5	3.0	713	2	08PU00_XANAC	08pu00 xanthomonas	1415	106	3.0	1729	2	05SPB1_CRYNE	05spb1 cryptococcu
1343	106.5	3.0	721	1	YCHD_SCHPO	09y7v2 schizosach	1416	106	3.0	1770	2	09X3P5_9PIRM	09x3p5 caldicellul
1344	106.5	3.0	756	2	06ITJ3_PHOPR	06itj3 photobacter	1417	106	3.0	2027	2	08UW52_FUGRU	08uw52 fugu rubrip
1345	106.5	3.0	792	2	05FR09_GLUOX	05fr09 gluconobact	1418	106	3.0	2111	2	04SOH1_TETNG	04soh1 tetraodon n



1419	106	3.0	2497	2	Q7YZ94_DROME
1420	106	3.0	2497	2	Q96806_DROME
1421	106	3.0	2797	2	Q81V22_HUMAN
1422	106	3.0	3183	2	Q8MLW2_DROME
1423	106	3.0	3198	2	Q917V8_DROME
1424	106	3.0	3201	2	Q9NDJ2_DROME
1425	106	3.0	4133	2	Q34EW3_DROME
1426	105.5	3.0	4133	2	Q3VXF0_9ACTO
1427	105.5	3.0	363	2	Q3W7T6_9ACTO
1428	105.5	3.0	378	2	Q19568_CAEL
1429	105.5	3.0	410	2	Q56AV3_9ACTO
1430	105.5	3.0	421	2	Q15329_HUMAN
1431	105.5	3.0	480	2	Q8SXX1_DROME
1432	105.5	3.0	480	2	Q3JCA9_NITOC
1433	105.5	3.0	513	2	Q9NHP8_DROME
1434	105.5	3.0	528	2	Q9ZPL6_TOBAC
1435	105.5	3.0	572	2	Q390V1_GEOMG
1436	105.5	3.0	606	2	Q2U6D9_ASFOR
1437	105.5	3.0	638	2	Q6TAX9_HUMAN
1438	105.5	3.0	650	2	Q5J347_CRYNE
1439	105.5	3.0	684	2	Q7XHM7_ORYSA
1440	105.5	3.0	688	2	Q916G6_LACDE
1441	105.5	3.0	721	2	Q591J1_CANAL
1442	105.5	3.0	738	2	Q4PB62_USTMA
1443	105.5	3.0	753	2	Q2Y2P2_GINTC
1444	105.5	3.0	814	2	Q55AJ1_DICDI
1445	105.5	3.0	817	1	VBP1_YEAST
1446	105.5	3.0	817	2	Q07229_YEAST
1447	105.5	3.0	818	2	Q418U1_GIBZE
1448	105.5	3.0	827	1	SSP2_PLAYO
1449	105.5	3.0	878	2	Q3U241_MOUSE
1450	105.5	3.0	887	2	Q239J3_DICDI
1451	105.5	3.0	915	2	Q4QRI6_BRARE
1452	105.5	3.0	974	2	Q3SIG5_RALME
1453	105.5	3.0	1015	2	Q4UMG2_XANCF
1454	105.5	3.0	1015	2	Q8P7N8_XANCF
1455	105.5	3.0	1015	2	Q97E41_CLOAB
1456	105.5	3.0	1082	2	Q4RUC4_TETNG
1457	105.5	3.0	1108	2	Q2KRF1_MAGGR
1458	105.5	3.0	1140	2	Q40BN7_9RHOB
1459	105.5	3.0	1206	2	Q9JRC4_ANAPH
1460	105.5	3.0	1223	2	Q9JRG6_ANAPH
1461	105.5	3.0	1232	2	Q8MXD2_DROME
1462	105.5	3.0	1240	2	Q9RQD5_ANAPH
1463	105.5	3.0	1253	2	Q9W111_DROME
1464	105.5	3.0	1299	2	Q9NSM8_HUMAN
1465	105.5	3.0	1371	2	Q3TWM2_MOUSE
1466	105.5	3.0	1371	2	Q8BV57_MOUSE
1467	105.5	3.0	1415	2	Q3YN49_BACTK
1468	105.5	3.0	1521	2	Q8CHS9_MOUSE
1469	105.5	3.0	1524	2	Q4P0B8_USTMA
1470	105.5	3.0	1744	2	Q6P4R1_HUMAN
1471	105.5	3.0	1748	1	BOLR_ELV
1472	105.5	3.0	1748	2	Q549I0_ELV
1473	105.5	3.0	1789	2	Q83883_9CALI
1474	105.5	3.0	1918	2	Q54F48_DICDI
1475	105.5	3.0	2112	2	Q80U93_MOUSE
1476	105.5	3.0	2133	2	Q7WRQ2_STAMU
1477	105.5	3.0	2364	2	Q4UR16_THEAN
1478	105.5	3.0	2590	2	Q7ONQ7_SITALA
1479	105	3.0	367	2	Q8U961_AGRIS
1480	105	3.0	412	2	Q7CTH6_AGRIS
1481	105	3.0	420	2	Q2YD66_BOVIN
1482	105	3.0	449	2	Q9H2K4_HUMAN
1483	105	3.0	464	2	Q431U3_SOLUS
1484	105	3.0	501	2	Q44CB9_CHRSL
1485	105	3.0	506	2	Q2RV63_RHORB
1486	105	3.0	516	2	Q54Z21_DICDI
1487	105	3.0	546	2	Q3MGJ3_ANAVT
1488	105	3.0	562	1	HEMA_IAPAP
1489	105	3.0	562	2	Q67144_9INFA
1490	105	3.0	566	2	Q55S21_CRYNE
1491	105	3.0	566	2	Q5KH03_CRYNE

Q7YZ94	dtrosophila
Q96806	dtrosophila
Q81V22	homo sapien
Q8MLW2	dtrosophila
Q917V8	dtrosophila
Q9NDJ2	dtrosophila
Q34EW3	rhodopsin
Q3VXF0	frankia sp.
Q3W7T6	frankia sp.
Q19568	caenorhabditis
Q56AV3	gordonia de
Q15329	homo sapien
Q8SXX1	dtrosophila
Q3JCA9	nitrosococc
Q9NHP8	dtrosophila
Q9ZPL6	nicotiana t
Q390V1	geobacter m
Q2U6D9	aspergillus
Q6TAX9	homo sapien
Q5J347	cryptococcu
Q7XHM7	oryza sativ
Q916G6	lactobacill
Q591J1	candida alb
Q4PB62	usciilago ma
Q2Y2P2	ginglymesto
Q55AJ1	dictyostell
P37370	saccharomyc
Q07229	saccharomyc
Q418U1	gibberella
Q01443	plasmodium
Q3U241	m nod-deriv
Q239J3	dictyostell
Q4QRI6	brachydanio
Q3SIG5	ratelocoma m
Q4UMG2	xanthomonas
Q8P7N8	xanthomonas
Q97E41	clostridium
Q4RUC4	clostridium
Q2KRF1	magnaporthe
Q40BN7	jannaschia
Q9JRC4	anaplasma p
Q9JRG6	anaplasma p
Q8MXD2	dtrosophila
Q9RQD5	anaplasma p
Q9W111	dtrosophila
Q9NSM8	homo sapien
Q3TWM2	mus musculu
Q8BV57	mus musculu
Q3YN49	bacillus th
Q8CHS9	mus musculu
Q4P0B8	usciilago ma
Q6P4R1	homo sapien
P35928	eyssium la
Q549I0	eyssium la
Q83883	normalk vir
Q54F48	dictyostell
Q80U93	mus musculu
Q7WRQ2	staphylococ
Q4UR16	theileria a
Q7ONQ7	giardia lam
Q8U961	agrobacteri
Q7CTH6	agrobacteri
Q2YD66	bos taurus
Q9H2K4	homo sapien
Q431U3	solibacter
Q44CB9	chromohalob
Q2RV63	rhodospirill
Q54Z21	dictyostell
Q3MGJ3	anabaena va
P373451	influenza a
Q67144	influenza a
Q55S21	cryptococcu
Q5KH03	cryptococcu

1492	105	3.0	585	2	Q8H501_ORYSA
1493	105	3.0	597	1	NP212_RAT
1494	105	3.0	604	2	Q6P7C8_RAT
1495	105	3.0	621	2	Q89ZB2_BACTN
1496	105	3.0	621	2	Q4SNW3_TETNG
1497	105	3.0	660	2	Q36613_9VIRU
1498	105	3.0	660	2	Q6J8F7_9VIRU
1499	105	3.0	660	2	Q6J8G3_9VIRU
1500	105	3.0	660	2	Q801R7_9VIRU

ALIGNMENTS

RESULT 1
Q6UX17_HUMAN
ID Q6UX17_HUMAN PRELIMINARY; PRT; 678 AA.
AC Q6UX17-
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VIT.
GN ORFNames=UNQ647;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh U., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL: AY358338; AAQ88704.1; --; mRNA.
DR HSSP: O43405; LJB1.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF03815; LCCL; 1.
DR Pfam: PF00092; VWA; 2.
DR PRINTS: PR00453; VWFADOMAIN.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00327; VWA; 2.
DR PROSITE: PSS0820; LCCL; 1.
DR PROSITE: PSS0234; VWF_A; 2.
DR SEQUENCE 678 AA; 73930 MW; 9870E75A218C686C CRC64;

Query Match	100.0%;	Score 3502;	DB 2;	Length 678;
Best Local Similarity	100.0%;	Pred. No. 3e-219;		
Matches 678;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MRTVVLITMAASVTEMLVLLVTGSHSNKETAKKIKPKFTVPOINCVDYAKGIIDPEFIY 60
DB	1	MRTVVLITMAASVTEMLVLLVTGSHSNKETAKKIKPKFTVPOINCVDYAKGIIDPEFIY 60
QY	61	KCPAGQODPKHYHYGTDVVAASVSGAIVHSGVLDNSGKILIVRAVAGSGYKGSYSNG 120
DB	61	KCPAGQODPKHYHYGTDVVAASVSGAIVHSGVLDNSGKILIVRAVAGSGYKGSYSNG 120

QY 121 VQSLSPRMRESFVLESKEPKGVTPSALTYSSSSKSPAQAQGETTKAYORPPIPGTTAQ 180  
 DB 121 VQSLSPRMRESFVLESKEPKGVTPSALTYSSSSKSPAQAQGETTKAYORPPIPGTTAQ 180  
 QY 181 PVTLMQLAVTVAVATPTTLPRPSPSAASTTSIPRPOSVGHRSQEMDLNSTATYTSQNR 240  
 DB 181 PVTLMQLAVTVAVATPTTLPRPSPSAASTTSIPRPOSVGHRSQEMDLNSTATYTSQNR 240  
 QY 241 PRADPGIORODPSGAFOKPVGADVSLGLVPEKEELSTQSLSPVSLGDPNCKIDLSFLIDG 300  
 DB 241 PRADPGIORODPSGAFOKPVGADVSLGLVPEKEELSTQSLSPVSLGDPNCKIDLSFLIDG 300  
 QY 301 STSICKRRFRIQKQLADVAQALDIDGAPGLMGVQYQNDPATEFNILKTHNSRDLKTAI 360  
 DB 301 STSICKRRFRIQKQLADVAQALDIDGAPGLMGVQYQNDPATEFNILKTHNSRDLKTAI 360  
 QY 361 EKTITRGGLSNVGRALISFTYTKNFKPSKANGRSKANPNNVVMVWDGMPDXYEASRLARES 420  
 DB 361 EKTITRGGLSNVGRALISFTYTKNFKPSKANGRSKANPNNVVMVWDGMPDXYEASRLARES 420  
 QY 421 GINIFFTTIGAAENKQYVVEPFAKAVCRTNGFYSLSHVQSWFGHAKTLQPLVKRVC 480  
 DB 421 GINIFFTTIGAAENKQYVVEPFAKAVCRTNGFYSLSHVQSWFGHAKTLQPLVKRVC 480  
 QY 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRIVLQFVNLTKFEISDTDTIRIGAVQYT 540  
 DB 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRIVLQFVNLTKFEISDTDTIRIGAVQYT 540  
 QY 541 YERLEGEFPGYSSKPIILNAIKRVGWSGTSGAALNLEOLFESKSPNKRKMLI 600  
 DB 541 YERLEGEFPGYSSKPIILNAIKRVGWSGTSGAALNLEOLFESKSPNKRKMLI 600  
 QY 601 TDRGSYDVVIRPAMAHLKGVITVTAIGVAAAOELEVIATHPADHSFVDEFDNLHQY 660  
 DB 601 TDRGSYDVVIRPAMAHLKGVITVTAIGVAAAOELEVIATHPADHSFVDEFDNLHQY 660  
 QY 661 VPRIIQNTCTEFSQSPN 678  
 DB 661 VPRIIQNTCTEFSQSPN 678  
 QY 661 VPRIIQNTCTEFSQSPN 678  
 DB 661 VPRIIQNTCTEFSQSPN 678  
 RESULT 2  
 Q9UDNO\_HUMAN PRELIMINARY; PRT; 693 AA.  
 ID Q9UDNO\_HUMAN PRELIMINARY; PRT; 693 AA.  
 AC Q9UDNO; Q96DM8;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 2.  
 DT 07-MAR-2006, entry version 26.  
 DE Hypothetical protein VIT (Hypothetical protein FLJ32210).  
 GN Name=VIT;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cordes M., Kalicki J., Ames M.;  
 RT "The sequence of Homo sapiens BAC clone Rpl1-29411.";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Waterston R.H.;  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Waterston R.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Wilson R.K.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 RN [5]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,  
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiraori A.,  
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
 RA Ninomiya K., Shibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,  
 RA Kamehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,  
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Musahiro K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shichahara N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Wakebe H.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hatao M., Omori Y., Okamoto S.,  
 RA Ohtsuki R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsuura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonCommercial License  
 CC  
 CC EMBL; AK056772; BAB71279.1; -; mRNA.  
 CC EMBL; AC007363; AAF19243.2; -; Genomic\_DNA.  
 CC  
 CC HSSP; O43405; IJBI.  
 CC HGNC; HGNC:12697; VIT.  
 DR InterPro; IPR004043; LCCL.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF03815; LCCL; 1.  
 DR Pfam; PF00092; VWA; 2.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR SMART; SM00603; LCCL; 1.  
 DR SMART; SM00327; VWA; 2.  
 DR PROSITE; PS50820; LCCL; 1.  
 DR PROSITE; PS50234; VWF; 2.  
 KM Hypothetical protein.  
 SQ SEQUENCE 693 AA; 75575 MW; 2DB8B2421F2D946D CRC64;  
 QY 99.5%; Score 3484.5; DB 2; Length 693;  
 Best Local Similarity 97.8%; Pred. No. 4.3e-218;  
 Matches 678; Conservative 0; Mismatches 0; Indels 15; Gaps 1;  
 QY 1 MTRVVLTMKASVEMFLVLLVGVHNSKETAKIKRPFVPPVINDVAKGIIDDEFIV 60  
 DB 1 MTRVVLTMKASVEMFLVLLVGVHNSKETAKIKRPFVPPVINDVAKGIIDDEFIV 60  
 QY 61 KCPAGCQDPKHYHYGTDVYASYSVCGAAVHSGVLNDSGKILVRKAVAGSGYKGSYNG 120  
 DB 61 KCPAGCQDPKHYHYGTDVYASYSVCGAAVHSGVLNDSGKILVRKAVAGSGYKGSYNG 120  
 QY 121 VQSLSPRMRESFVLESKEPKGVTPSALTYSSSSKSPAQAQGETTKAYORPPIPGTTAQ 180  
 DB 121 VQSLSPRMRESFVLESKEPKGVTPSALTYSSSSKSPAQAQGETTKAYORPPIPGTTAQ 180  
 QY 181 PVTLMQLAVTVAVATPTTLPRPSPSAASTTSIPRPOSVGHRSQEMDLNSTATYTSQNR 240  
 DB 181 PVTLMQLAVTVAVATPTTLPRPSPSAASTTSIPRPOSVGHRSQEMDLNSTATYTSQNR 240

```

QY 241 PRADPGIQRDPGSAFAQKPVGADVSL-----GLVPKEELSTOSLEPVSL 285
Db 241 PRADPGIQRDPGSAFAQKPVGADVSLGEMDSWKRGSVLDEGLVPKEELSTOSLEPVSL 300
QY 286 GDPNCKIDLSLIDGSTIGKRRFRIOKQOLLADVAQALDIPAGPLMGVVOYGNDPATHF 345
Db 301 GDPNCKIDLSLIDGSTIGKRRFRIOKQOLLADVAQALDIPAGPLMGVVOYGNDPATHF 360
QY 346 NLKHTNSRDLKTAIEKTORGGLSNVGRALSFVTKNPFSSKANGNRSGAPNVVVVMDGW 405
Db 361 NLKHTNSRDLKTAIEKTORGGLSNVGRALSFVTKNPFSSKANGNRSGAPNVVVVMDGW 420
QY 406 PTDKVEASRLARSGINIFITTEGAENKQYVVEBNPANKAVCRITNGFYSLHVOSWF 465
Db 421 PTDKVEASRLARSGINIFITTEGAENKQYVVEBNPANKAVCRITNGFYSLHVOSWF 480
QY 466 GLHKTLOPLVKRVCDTDLRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNLTKEF 525
Db 481 GLHKTLOPLVKRVCDTDLRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNLTKEF 540
QY 526 EISPTDRIGAVOYTYEORLEFGFDKYSKSKPDILNAIKRVGWSGCTGTGAINFALBOL 585
Db 541 EISPTDRIGAVOYTYEORLEFGFDKYSKSKPDILNAIKRVGWSGCTGTGAINFALBOL 600
QY 586 FKSKSPNKRKLMILITDGRSYDVRIIPAMAHLKGVITTYAIGVMAAOEBLEVIATHPAR 645
Db 601 FKSKSPNKRKLMILITDGRSYDVRIIPAMAHLKGVITTYAIGVMAAOEBLEVIATHPAR 660
QY 646 DHSFVDEFDNLHOYVRRIITNICTEFNSOPRN 678
Db 661 DHSFVDEFDNLHOYVRRIITNICTEFNSOPRN 693

RESULT 3
Q96DT1_HUMAN PRELIMINARY; PRT; 656 AA.
ID Q96DT1_HUMAN
AC Q96DT1
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Vitrin.
GN Name=VIT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Ren Z.-X., Liu J.G., Mayne R.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial license
CC -----
DR EMBL: AF063833; AAL18263.1; -, mRNA.
DR HSSP: O43405; 1JBI.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF03815; LCCL.1.
DR Pfam: PF00092; VMA; 2.
DR PRINTS: PR00453; VWFADOMAIN..
DR SMART: SM00603; LCCL.1.
DR SMART: SM00327; VMA; 2.
DR PROSITE: PS00820; LCCL.1.
DR PROSITE: PS50234; VWF_A; 2.
DR SEQUENCE 656 AA; 71768 MW; E242E0DFFB07CF2C CRC64;

Query March 95.5%; Score 3344; DB 2; Length 656;
Best Local Similarity 96.0%; Pred. No. 5.7e-209;
Matches 651; Conservative 1; Mismatches 4; Indels 22; Gaps 1;

```

```

QY 1 MRTVLTMKASVIEMLVLLVTGVHSNKETAKKIKRKFTVPOINCVDKAKIIDPEFIV 60
Db 1 MRTVLTMKASVIEMLVLLVTGVHSNKETAKKIKRKFTVPOINCVDKAKIIDPEFIV 60
QY 61 KCPAGCDDPKYHYGTDVYASYSVCGAAGVHGLDNGSGKILYRKVAGOSGYKGSYNG 120
Db 61 KCPAGCDDPKYHYGTDVYASYSVCGAAGVHGLDNGSGKILYRKVAGOSGYKGSYNG 120
QY 121 VQSLSPRMRESFVLESKRKKGVTPSALTYSSSKSPAQAQETTKAYORPPIPGTTAQ 180
Db 121 VQSLSPRMRESFVLESKRKKGVTPSALTYSSSKSPAQAQETTKAYORPPIPGTTAQ 180
QY 181 PVTLMQALATVAVAFTTLPSPSPASATTSIPRPOSVGRSQEMDLMTATYSSQNR 240
Db 181 PVTLMQALATVAVAFTTLPSPSPASATTSIPRPOSVGRSQEMDLMTATYSSQNR 240
QY 241 PRADPGIQRDPGSAFAQKPVGADVSLGLVPKEELSTOSLEPVSLGDPNCKIDLSFLIDG 300
Db 241 PRADP-----GLVPKEELSTOSLEPVSLGDPNCKIDLSFLIDG 278
QY 301 STSIGKRRFRIOKQOLLADVAQALDIPAGPLMGVVOYGNDPATFNLKHTNSRDLKTAI 360
Db 279 STSIGKRRFRIOKQOLLADVAQALDIPAGPLMGVVOYGNDPATFNLKHTNSRDLKTAI 338
QY 361 EKITRGRGLSNVGRALSFVTKNPFSSKANGNRSGAPNVVVVMDGWPTDKVEASRLARSG 420
Db 339 EKITRGRGLSNVGRALSFVTKNPFSSKANGNRSGAPNVVVVMDGWPTDKVEASRLARSG 398
QY 421 GINIFPTTIGAAENKQYVVEBNPANKAVCRITNGFYSLHVOSFGIHKTLQPLVKRVCD 480
Db 399 GINIFPTTIGAAENKQYVVEBNPANKAVCRITNGFYSLHVOSFGIHKTLQPLVKRVCD 458
QY 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNLTKEFISDPTDRIGAVOYT 540
Db 459 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNLTKEFISDPTDRIGAVOYT 518
QY 541 YEORLFEGFDKYSKSKPDILNAIKRVGWSGCTGTGAINFALBOLFKSKSPNKRKLMILI 600
Db 519 YEORLFEGFDKYSKSKPDILNAIKRVGWSGCTGTGAINFALBOLFKSKSPNKRKLMILI 578
QY 601 TDRGSYDVRIIPAMAHLKGVITTYAIGVMAAOEBLEVIATHPARDHSFVDEFDNLHOY 660
Db 579 TDRGSYDVRIIPAMAHLKGVITTYAIGVMAAOEBLEVIATHPARDHSFVDEFDNLHOY 638
QY 661 VPRITONICTEFNSOPRN 678
Db 639 VPRITONICTEFNSOPRN 656

RESULT 4
Q37Z47_MOUSE PRELIMINARY; PRT; 650 AA.
ID Q37Z47_MOUSE
AC Q37Z47
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Adult inner ear cDNA, RIKEN full-length enriched library,
DE clone: F930022K14 product: vitrin, full insert sequence.
DE Name=VIT;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44 (1999).
[2]

```

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=inner ear;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
RA Oyama R., Ravasi T., Lenhard B., Wells S., Gough J., Frith M.C., Maeda N.,  
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,  
RA Davis M.J., Wilmshaw L.G., Aldonis V., Allen J.E.,  
RA Ambesi-Impombato A., Apweiler R., Attaliya R.N., Bailey T.L.,  
RA Bansal S., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
RA Guernicelli S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hall D., Humeiri L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jaki M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Ljung S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuda H., Matuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Motegut-Taber S., Mulder N., Nakano N., Nakachi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
RA Schombach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,  
RA Tanno K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Ye J.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hilde W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Karayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imanura K., Itoh M., Kato T., Kawaji H., Kawaguchi N.,  
RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Niimura N.,  
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=inner ear;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RA RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense transcription in the mammalian transcriptome.";  
RL Science 309:1564-1566(2005).  
[4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=inner ear;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Guernicelli S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawai H., Kawasawa Y., Kedziercki R.M., King B.L.,  
RA Kanagawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagasawa T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Saitana R., Schneider C., Sempke C.A., Setou M., Shimada K.,  
RA Sultana R., Takemura Y., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Willestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilmshaw L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Myazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yamanishi A., Yoshino M., Waterson R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=inner ear;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana H.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Wilmshaw L.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Baldarelli R., Bojunga N., Carninci P., de Bono B.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guernicelli S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Monbaets P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Wilmshaw L., Wilmshaw L.,  
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=inner ear;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=inner ear;  
RX MEDLINE=20530913; PubMed=11078661; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Kono H., Akiyama U., Nishi K., Kitsuui T., Tashiro H., Itoh M.,  
RA Sami N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=inner ear;  
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Hori F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,  
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Niimura N.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC EMBL: AK158117; BAE34363.1; -; mRNA.  
DR MGI: MGI1921449; Vlt.



```

Db      510 QYTYEQRLOFGFDKYNKADILSLAIRVGYWSGTGTGAALIQVLEQLFKSKRNKRW 569
QY      598 ILITDGSYDVRIRPAMAHLKGVITYAIGVAMAQDELEVIATHPARHSPFVDEPNL 657
Db      570 ILITDGSYDVRIRPAMAHLKGVITYAIGVAMAQDELEVIATHPARHSPFVDEPNL 629
QY      658 HQYVPRRIIONICTEFSNQP RN 678
Db      630 YKIAPRRIIONICTEFSNQP RN 650

RESULT 6
Q9SL12_BOVIN  PRELIMINARY;  PRT;  652 AA.
ID  Q9SL12_BOVIN  PRELIMINARY;  PRT;  652 AA.
AC  Q9SL12;
DT  01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT  01-MAR-2002, sequence version 2.
DT  07-FEB-2006, entry version 16.
DE  Vitrin.
GN  Name=VIT;
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC  Pecora; Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Retina;
RA  Ren Z.-X., Liu J.G., Wayne R.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NonDerivs License
CC  -----
EMBL: AF063832; AALJ8262.2; -, mRNA.
DR  HSSP: O43405; 1JBI.
DR  InterPro: IPR004043; LCCL.
DR  InterPro: IPR002035; VWF_A.
DR  Pfam: PF03815; LCCL; 1.
DR  Pfam: PF00092; VMA; 2.
DR  PRINTS: PR00453; VWFADOMAIN.
DR  SMART: SM00603; LCCL; 1.
DR  SMART: SM00327; VMA; 2.
DR  PROSITE: PS50820; LCCL; 1.
DR  PROSITE: PS50234; VWF_A; 2.
SQ  SEQUENCE 652 AA; 70873 MW; 3512421CA987C51 CRC64;

Query Match      80.5%; Score 2818; DB 2; Length 652;
Best Local Similarity 79.8%; Pred. No. 1e-174;
Matches 541; Conservative 49; Mismatches 62; Indels 26; Gaps 2;

QY      1 MRTVLTMRKASVLEMPFLVLTGVSHNKETAKIKRPFVTVPQINCVDKAGKIIDPEFIV 60
Db      1 MGIVLTMRKASVLEMPFLVLTGVSHNKETAKIKRPFVTVPQINCVDKAGKIIDPEFIV 60
QY      61 KCPAGCDDPKYHYGTVDVYASVSSVCAVAHSGVLDNSGGKILVRKVAAGSGYKGSYNG 120
Db      61 KCPAGCDDPKYHYGTVDVYASVSSVCAVAHSGVLDNSGGKILVRKVAAGSGYKGSYNG 120
QY      121 VQSLSPRMRBSFVLESKPKKGVTSALTYSSSKSPAAQAGTTAYQRPPIPGTAAQ 180
Db      121 VQSLSPRMRBSFVLESKPKKGVTSALTYSSSKSPAAQAGTTAYQRPPIPGTAAQ 180
QY      181 PVLMLQALATVAATPTTLPRPSPASATTSIPRPOVGHRSQEMDLMTATATYSSQNR 240
Db      181 PVLMLQALATVAATPTTLPRPSPASATTSIPRPOVGHRSQEMDLMTATATYSSQNR 240
QY      241 PRADPGIQRDDPSGAFQKPVGADVSLGLVPEKEELSTQSLSPVSLDGNCKIDLSFLIDG 300
Db      241 PRADPGIQRDDPSGAFQKPVGADVSLGLVPEKEELSTQSLSPVSLDGNCKIDLSFLIDG 300
QY      227 --GSP-----ALMKPESVLLDAGFVPKEELSTQSLSPASQDPSCKVDLSFLIDG 274
Db      227 --GSP-----ALMKPESVLLDAGFVPKEELSTQSLSPASQDPSCKVDLSFLIDG 274
QY      301 STSGKRFRRIQKOLLADVQALDIGAGPLMGVGVGDNPATFNKTKHTNSRDLKTAI 360
Db      301 STSGKRFRRIQKOLLADVQALDIGAGPLMGVGVGDNPATFNKTKHTNSRDLKTAI 360

```

```

Db      275 SSSIGRRFRRIQKOLLADVQALDIGAPBPLMGVGVGDNPATFNKTKHTNSQDVKAII 334
QY      361 EKITRGGLSNVGRASIFVTKNFFSKANGRSGAPVNVVVVWDGWPDTDEKESRLARS 420
Db      335 EKISQKGLSNAGRASIFVTKNFFSKANGRSGAPVNVVVVWDGWPDTDEKESRLARS 394
QY      421 GINIFPITTEGAANEKQYVEPNFANKAVCRTNGFYSLHVOSFGLHKTLOPLVKRVD 480
Db      395 GVINIFPITTEGAANEKQYVEPNFANKAVCRTNGFYSLHVOSFGLHKTLOPLVKRVD 454
QY      481 TDRLACKTCNLNADIGFVIDGSSSVGTGNFRTVLQFVNLTKEEISPTDRIGVOYT 540
Db      455 TDRLACKTCNLNADIGFVIDGSSSVGTGNFRTVLQFVNLTKEEISPTDRIGVOYT 514
QY      541 YEORLEFGFDKYSKSKDIINAIKRVGWSGTSTGAINFALAEQLFKSKPNKRKLMILI 600
Db      515 YEORLEFGFDKYSKSKDIINAIKRVGWSGTSTGAINFALAEQLFKSKPNKRKLMILI 574
QY      601 TDGRSYDVRIRPAMAHLKGVITYAIGVAMAQDELEVIATHPARDHSPFVDEPNLHOY 660
Db      575 TDGRSYDVRIRPAMAHLKGVITYAIGVAMAQDELEVIATHPARDHSPFVDEPNLHYK 634
QY      661 VPRRIIONICTEFSNQP RN 678
Db      635 VPRRIIONICTEFSNQP RN 652

RESULT 7
Q8K047_MOUSE  PRELIMINARY;  PRT;  650 AA.
ID  Q8K047_MOUSE  PRELIMINARY;  PRT;  650 AA.
AC  Q8K047;
DT  01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT  01-OCT-2002, sequence version 1.
DT  07-FEB-2006, entry version 18.
DE  Vitrin.
GN  Name=Vit;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Eye;
RA  MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Lottelino N.A., Peters G.J., Abramson R.D., Mallat S.J.,
RA  Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA  Schenck A., Schein U.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RL  and mouse cDNA sequences.";
RN  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Eye;
RA  Director MGC Project;
RL  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NonDerivs License

```

```

CC -----
DR EMBL; BC034120; AAH34120.1; -; mRNA.
DR HSSP; 043405; IJBI.
DR Ensembl; ENSMUSG00000024076; Mus musculus.
DR MGI; MGI:1921449; Vlt.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VMPADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VMA; 2.
DR SEQUENCE 650 AA; 70699 MW; 1641623E11003B4E CRC64;

Query Match      80.0%; Score 2801; DB 2; Length 650;
Best Local Similarity 80.5%; Pred. No. 1.3e-173;
Matches 548; Conservative 40; Mismatches 59; Indels 34; Gaps 5;

QY 1 MRVAVLTMKASVIMFVLVLTGVHNSKETAKIKRPFTVPOINCVDKAKIIDPEFIV 60
DB 1 MGIVPPTMKASVIEVLVLTGVHNSKETAKIKRPFTVPOINCVDKAKIIDPEFIV 60
QY 61 KCPAGCDDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGKILVRKVAAGSGYKYSNG 120
DB 61 KCPAGCDDPKHYVGTVDVYASVSSVCGAAVHSGVLDNSGKILVRKVAAGSGYKYSNG 120
QY 121 VQSLSPRWRESFVLESKPKKGYTPBALTYSSSKSAQAAGTTAYAGPPITPTAQ 180
DB 121 VQSLSPRWRESFVLESKPKKGYTPBALTYSSSKSAQAAGTTAYAGPPITPTAQ 180
QY 121 VQSLSPRWRESFVLESKPKKGYTPBALTYSSSKSAQAAGTTAYAGPPITPTAQ 180
DB 121 VQSLSPRWRESFVLESKPKKGYTPBALTYSSSKSAQAAGTTAYAGPPITPTAQ 180
QY 181 PVTLMQIAVAVATPTLPRPSPSAATSTIRPQSVGHRSGDEM--DLMSATATYSS 237
DB 181 PVTLMQIAVAVATPTLPRPSPSAATSTIRPQSVGHRSGDEM--DLMSATATYSS 237
QY 181 PVTLMQIAVAVATPTLPRPSPSAATSTIRPQSVGHRSGDEM--DLMSATATYSS 237
DB 181 PVTLMQIAVAVATPTLPRPSPSAATSTIRPQSVGHRSGDEM--DLMSATATYSS 237
QY 238 QNRPRADPGIORQDPGSAFQPGVADVSLGLVPEKEELSTQSLPEVSLGDPNCKIDLSFL 297
DB 238 QNRPRADPGIORQDPGSAFQPGVADVSLGLVPEKEELSTQSLPEVSLGDPNCKIDLSFL 297
QY 232 -----PG-----PVLLD--SGFVPEKEELSTQSSBPVQGDNDCKIDLSFL 269
DB 232 -----PG-----PVLLD--SGFVPEKEELSTQSSBPVQGDNDCKIDLSFL 269
QY 298 IDGSTSGKRRFRIOKOLLADVAADLIDGAPGLMGVVOYGDNDATHTNLKTHNSDLK 357
DB 298 IDGSTSGKRRFRIOKOLLADVAADLIDGAPGLMGVVOYGDNDATHTNLKTHNSDLK 357
QY 270 IDGSTSGKRRFRIOKOLLADVAADLIDGAPGLMGVVOYGDNDATHTNLKTHNSDLK 329
DB 270 IDGSTSGKRRFRIOKOLLADVAADLIDGAPGLMGVVOYGDNDATHTNLKTHNSDLK 329
QY 358 TAIKTIORGGLSNVGRALISFVTNPFPSKANGNSGAPNVVWVWDGPTDKVEASRLA 417
DB 358 TAIKTIORGGLSNVGRALISFVTNPFPSKANGNSGAPNVVWVWDGPTDKVEASRLA 417
QY 330 TAIKTIORGGLSNVGRALISFVTNPFPSKANGNSGAPNVVWVWDGPTDKVEASRLA 389
DB 330 TAIKTIORGGLSNVGRALISFVTNPFPSKANGNSGAPNVVWVWDGPTDKVEASRLA 389
QY 418 RESGINIFITIEGAENKQYVEPNFANKAVCRINGFYSLHVQSWFGLHKTLOPLVKR 477
DB 418 RESGINIFITIEGAENKQYVEPNFANKAVCRINGFYSLHVQSWFGLHKTLOPLVKR 477
QY 390 RESGINIFITIEGAENKQYVEPNFANKAVCRINGFYSLHVQSWFGLHKTLOPLVKR 449
DB 390 RESGINIFITIEGAENKQYVEPNFANKAVCRINGFYSLHVQSWFGLHKTLOPLVKR 449
QY 478 VCDTRDLACSTKCNASDIDGIVIDGSSVGTGNRTVLOFTNLTKEFEISDTRIGAV 537
DB 478 VCDTRDLACSTKCNASDIDGIVIDGSSVGTGNRTVLOFTNLTKEFEISDTRIGAV 537
QY 450 VCDTRDLACSTKCNASDIDGIVIDGSSVGTGNRTVLOFTNLTKEFEISDTRIGAV 509
DB 450 VCDTRDLACSTKCNASDIDGIVIDGSSVGTGNRTVLOFTNLTKEFEISDTRIGAV 509
QY 538 QYTEQRLERFGFDKYSKPDILNAIKVGYWVSGSTGAIINPABLEOFKSKNPKRKL 597
DB 538 QYTEQRLERFGFDKYSKPDILNAIKVGYWVSGSTGAIINPABLEOFKSKNPKRKL 597
QY 510 QYTEQRLERFGFDKYSKPDILNAIKVGYWVSGSTGAIINPABLEOFKSKNPKRKL 569
DB 510 QYTEQRLERFGFDKYSKPDILNAIKVGYWVSGSTGAIINPABLEOFKSKNPKRKL 569
QY 598 ILITDGSYDVRIPAMAHLKGVITYTAIGVAMAQOELEVIATHPARSHFVDEEDNL 657
DB 598 ILITDGSYDVRIPAMAHLKGVITYTAIGVAMAQOELEVIATHPARSHFVDEEDNL 657
QY 570 ILITDGSYDVRIPAMAHLKGVITYTAIGVAMAQOELEVIATHPARSHFVDEEDNL 629
DB 570 ILITDGSYDVRIPAMAHLKGVITYTAIGVAMAQOELEVIATHPARSHFVDEEDNL 629
QY 658 HQYVPRITONCTEFNSOPRN 678
DB 658 HQYVPRITONCTEFNSOPRN 678
QY 630 YKIAPRITONCTEFNSOPRN 650
DB 630 YKIAPRITONCTEFNSOPRN 650

```

```

AC 09CYZ1;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE 10, 11 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:2810429K11 product:VITRIN, full insert sequence.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilmink L.G., Aldins V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Cluttenbuck D.R.,
RA Crowe M.L., Dalia E., Dairymple B.P., de Bono B., Della Gatta G.,
RA di Bernhardt D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Guignicci S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jact M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Lium S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Roost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeig K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Tesardate R.D., Liu E.T., Bruste V., Quackenbush J.,
RA Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arikawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawasashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Teganu M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RA (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;

```







Db 390 RESGNNFFITTEGAERDIOHVEBPGRSAKVCFTNGFYSFNNVSMLSLHKTOPLVKR 449  
 Qy 478 VCDTRDLACSKTCLNSADIGFVIDSSSGYGTGNTFTVLOFNTLTKREEISPTDRIGAV 537  
 Db 450 VCDTRDLACSKTCLNSADIGFVIDSSSGYGTGNTFTVLOFNTLTKREEISPTDRIGAV 509  
 Qy 538 QYTTQORLEFGDKYSSKPDINAIRVGYMSGTSTAINFALFQEPKSKPKRKLM 597  
 Db 510 QYTTQORLEFGDKYSSKPDINAIRVGYMSGTSTAINFALFQEPKSKPKRKLM 569  
 Qy 598 ILITDGRSYDPRIPAMAHKGVITVAIGVMAAOEELFVATAPADHSFVDEPNTL 657  
 Db 570 ILITDGRSYDPRIPAMAHKGVITVAIGVMAAOEELFVATAPADHSFVDEPNTL 629  
 Qy 658 HOYVPRRIIONICTEFNSQPRN 678  
 Db 630 YKIAPRIIONICTEFNSQPRN 650  
 RESULT 9  
 Q8BQ41 MOUSE PRELIMINARY: PRT: 628 AA.  
 AC Q8BQ41-  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 19.  
 DE 12 days embryyo spinal ganglion cDNA, RIKEN full-length enriched  
 DE library, clone:DI30059M21 product:VIRIN homolog.  
 GN Name=Vlt;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Method Enzymol. 303:19-44(1999).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX PubMed=1641072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impombato A., Apweiler R., Atturaliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chaik A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgi-Hemming P., Gingeras T.R., Gojovic T., Green R.E.,  
 RA Guinacich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Lium S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottacuti-Tabar S., Mulder N., Nakano N., Nakanchi H., Ng P.,  
 RA Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,  
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schombach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shiba Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,  
 RA Tammoja K., Tan S.L., Tang S., Taylor W.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeai K.,

RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida Y., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashita N.,  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX PubMed=1641073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 RG (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Oosato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojovic T.,  
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Choehia C., Corbani L.B., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Girmond S., Gustincich S., Hirokawa N., Jackson J.D., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedziercki R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Saitana R., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yaenunshi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojovic T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirini L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaets P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN [6]  
 RP NCLEOTIDE SEQUENCE  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [7]  
 RP NCLEOTIDE SEQUENCE  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Katsunaka T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,  
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "AIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [8]  
 RP NCLEOTIDE SEQUENCE  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RA Aachti J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Hori F., Imcanti K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohato N., Okazaki Y.,  
 RA Saito R., Satoh K., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 CC  
 CC EMBL: AK051606; BAC34688.1; -; mRNA.  
 CC  
 CC HSSP: O43405; IJBI.  
 CC  
 CC DR Ensembl: ENSMUSG00000024076; Mus musculus.  
 CC  
 CC MGI: MGI:1921449; Vlt.  
 CC  
 CC DR GO: GO:0005615; C:extracellular space; RCA.  
 CC  
 CC DR InterPro: IPR004043; LCCL.  
 CC  
 CC DR InterPro: IPR002035; VWF\_A.  
 CC  
 CC DR Pfam: PF03815; LCCL; 1.  
 CC  
 CC DR Pfam: PF00092; VMA; 2.  
 CC  
 CC DR PRINTS: PR00453; VWFADOMAIN.  
 CC  
 CC DR SMART: SM00603; LCCL; 1.  
 CC  
 CC DR SMART: SM00327; VMA; 2.  
 CC  
 CC DR PROSITE: PS50820; LCCL; 1.  
 CC  
 CC DR PROSITE: PS50234; VMA; 2.  
 CC  
 CC SQ SEQUENCE 628 AA; C96CAACEB9E72480 CEC64;  
 Query Match 76.6%; Score 2682; DB 2; Length 628;  
 Best local similarity 77.7%; Pred. No. 7.1e-166;  
 Matches 529; Conservative 39; Mismatches 57; Indels 56; Gaps 6;

QY 1 MRYTVLTMKASVEMFLVLTGVSNSKETAKIKRKFYVPOINCVKAKGIIDPEFIV 60  
 DB 1 MGIVPTMKASVIEVL-----AVPQINCCVVKKGKIIINPEFV 38  
 QY 61 KCPAGCDDPKHYVGTVDYASYSVCGAAVHSGVLDNSGKILVRKYVAGSGYKGSYNG 120  
 DB 39 KCPAGCDDPKHYVGTVDYASYSVCGAAIHSGVLDNSGKILVRKYVAGSGYKGSYNG 98

QY 121 VQSLSPRMESFIVLESKPKKGVTPSALTYSSSKSPAQAQGETTKAYORPPIPGTTAQ 180  
 DB 99 VQSLSPRMESFIVLESKPKKGVTPSALTYSSSKSPAQAQGETTKAYORPPIPGTTAQ 158  
 QY 181 PVTLMQALNTVAVAPPTLPRSPSAASTSIIPROSVCHROEM---DLWSTATYSS 237  
 DB 159 PVTLMQALNTVAVAPPTLPRSPSAASTSIIPROSVCHROEM---DLWSTATYSS 209  
 QY 238 QNRPRADPGIQORPSCGAFFQKPVGADVSLGLVPKEELSTQSLPVLGDPNCKIDLSFL 297  
 DB 210 -----PG-----PVLVD--SGFVPKELSTQSLPVLGDPNCKIDLSFL 247  
 QY 298 IDGSTIGKRRFRIQQLADVAQALDIDGPAFLMGVVOYGDNPATHPNLKHTNSBDLK 357  
 DB 248 IDGSTIGKRRFRIQQLADVAQALDIDGPAFLMGVVOYGDNPATHPNLKHTNSBDLK 307  
 QY 358 TALEKTORGSLSNVRALSFVTKNPFSSKANGRSAPVNVVYVGVGDPDKVEASRLA 417  
 DB 308 TALEKTORGSLSNVRALSFVTKNPFSSKANGRSAPVNVVYVGVGDPDKVEASRLA 367  
 QY 418 RESGINIFFTTIGAAENKQYVVEPNFANKAVCRITNGFYSLHVQSMFGIHKTLQPLVXR 477  
 DB 368 RESGINIFFTTIGAAENKQYVVEPNFANKAVCRITNGFYSLHVQSMFGIHKTLQPLVXR 427  
 QY 478 VCDTDLRACSKTCLNSADIGFVIDSSSVGTGNFRTVLOFTNLTKBEFISDTDRIGAV 537  
 DB 428 VCDTDLRACSKTCLNSADIGFVIDSSSVGTGNFRTVLOFTNLTKBEFISDTDRIGAV 487  
 QY 538 QYVYBRLRLEGFPKYSKSDIILNAIKRVGWSGCTSGAINALBOLFPKSKPNRKLM 597  
 DB 488 QYVYBRLRLEGFPKYSKSDIILNAIKRVGWSGCTSGAINALBOLFPKSKPNRKLM 547  
 QY 598 ILITDGRSYDVRIIPMAAHLKGVITVAIGVAAQEELEVIATPHARDHSFVDEFDNL 657  
 DB 548 ILITDGRSYDVRIIPMAAHLKGVITVAIGVAAQEELEVIATPHARDHSFVDEFDNL 607  
 QY 658 HQVVPRIQNTCTEENSOPRN 678  
 DB 608 YKIAPRIQNTCTEENSOPRN 628

RESULT 10  
 Q5NTW9\_CHICK PRELIMINARY; PRT; 748 AA.  
 AC Q5NTW9;  
 DT 01-FEB-2005, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2005, sequence version 1.  
 DE 07-FEB-2006, entry version 8.  
 DE Aklirin precursor.  
 GN Name=Akl;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP NCLEOTIDE SEQUENCE.  
 RX PubMed=15765510; DOI=10.1002/dvdy.20303;  
 RA Ahsan M., Ohta K., Kuriyama S., Tanaka H.;  
 RT "Novel soluble molecule, Aklirin, is expressed in the embryonic chick  
 RT eyes and exhibits heterophilic cell-adhesion activity";  
 RL Dev. Dyn. 233:95-104(2005).  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 CC  
 CC EMBL: AB185956; BAD81032.1; -; mRNA.  
 CC  
 CC DR InterPro: IPR004043; LCCL.  
 CC  
 CC DR InterPro: IPR002035; VWF\_A.  
 CC  
 CC DR Pfam: PF03815; LCCL; 1.  
 CC  
 CC DR Pfam: PF00092; VMA; 2.  
 CC  
 CC DR PRINTS: PR00453; VWFADOMAIN.  
 CC  
 CC DR SMART: SM00603; LCCL; 1.

DR SMART; SM00327; VMA; 2.  
 DR PROSITE; PS50820; LCCL; 1.  
 DR PROSITE; PS50234; WMPA; 2.  
 FT SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 1 19 Potential.  
 748 AA; 81400 MW; 16299BRCDF8570E CRC64;

Query Match 66.0%; Score 2311.5; DB 2; Length 748;  
 Best Local Similarity 60.4%; Pred. No. 1.2e-141;  
 Matches 457; Conservative 86; Mismatches 120; Indels 93; Gaps 8;

QY 8 MKASYEMFVLVLTGCHSNKETAKIRPKRTVQINCVDYAKGIIIDPEFIKVPACQ 67  
 DB 1 MKASYIAFEGVLITCTYAAKEATKTKKAEIYIQQIDVDYAGKIIIDPEFIKVPACQ 60  
 QY 68 DKYHVTGTVYASVCGAAVHSGVDNSGKILVRYAGOSGKYSNGVOSLSP 127  
 DB 61 DKYKVTGTVIYASVSSACSAIHSAGALDNTGKILVRYAGOSGKYSNGVOSLSP 120  
 QY 128 RWRESFVLESKPKKGVTPSALTYSSSKSPAA----- 160  
 DB 121 RWRESFVLESKPKKGVTPSALTYSSSKSPAA----- 160  
 QY 161 QAGETT-KAYQRPPIPGTTAOPVITLMQLAVTAVATPT-----TLRPSPSAASSTSI 213  
 DB 181 EOGDTRVRYQTSVPVMPPTQ-----MAATTPPTTTTDPSTTPEKPTTPTTPTT 233  
 QY 214 -----PRP-----OSVGRSQEMDLMSTATYTSQ 238  
 DB 234 TDSAAKRRPGLQVRDVGSSVHAYSVVAAASRQVQASQGLNKAFFGTISASNR 293  
 QY 239 NRPRADPGIQRQDPSGAAPQKPVGADVL-----GLVPKEELSTOSLEP 282  
 DB 294 NILPRNAGIQROEPV-ATVRRPAGSPALAIETDLMKPGSPFPDGFASKELNKLPLEA 352  
 QY 283 VSLDPPNCKILSFLIDSTSIKRRFRIOQLADVAQALDIGPAGILMGVQYGNPA 342  
 DB 353 TSQGNPSCKVLPFLMDGWSIGKRRFQLOKFLINVAHAGINNAGFLMGVQYGDPS 412  
 QY 343 TFFNLKTTNRDILKTAIEKTIRQGLSNVGRALSFVTKNFFSKANGRSAGPNNVVMV 402  
 DB 413 TFFNLKTTNRDILKTAIEKTIRQGLSNVGRALSFVTKNFFSKANGRSAGPNNVVMV 472  
 QY 403 DGMPTDYVEASRLARESGINIFLTITGAAENKQYVVEBNFANKAVCRNTEGYSLHVQ 462  
 DB 473 DGMPTDYVEASRLARESGINIFLTITGAAENKQYVVEBNFANKAVCRNTEGYSLHVQ 532  
 QY 463 SWFGLHKTLPVLRVCTDRLACSKTCLNAGDIGFVTDGSSVGTGNFRTVLOFTNLT 522  
 DB 533 SWFGLHKTLPVLRVCTDRLACSKTCLNAGDIGFVTDGSSVGTGNFRTVLOFTNLT 592  
 QY 523 KEFISIDTDRIGAVQVYEQRLFEFGFDKYSKPDILNAIKRVGWSGSGTGAIPAL 582  
 DB 593 KEFISIDTDRIGAVQVYEQRLFEFGFDKYSKPDILNAIKRVGWSGSGTGAIPAL 652  
 QY 583 EQLFKSKPKNRKMLIITDGRSYDVARIIPMAAHLKGVITTYAIGVMAAOELEVIAIH 642  
 DB 653 EQLFKSKPKNRKMLIITDGRSYDVARIIPMAAHLKGVITTYAIGVMAAOELEVIAIH 712  
 QY 643 PARHSPFVDFEFDNLHQVVRPIIIONICTEFPNSOPRN 678  
 DB 713 PDKEHSFFVDFEFDNLHQVVRPIIIONICTEFPNSOPRN 748

RESULT 11  
 Q4RP27 TETNG  
 ID Q4RP27 TETNG PRELIMINARY; PRT; 680 AA.  
 AC Q4RP27;  
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Chromosome 17 SCAP15006, whole genome shotgun sequence. (Fragment).  
 GN ORNames=GSTING0030857001;

OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 CX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed:15496914; DOI=10.1038/nature03025;  
 RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,  
 RA Mancel E., Bouneau L., Fischer C., Ozouf-Costaz C., Benoit A.,  
 RA Maucel S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,  
 RA Crund C., Duprat S., Brothier J.-P., Gouzy J.,  
 RA Parra G., Landier G., Chapple C., McKernan K.J., McMan P., Bosak S.,  
 RA Kellis M., Wolf J.-N., Guigo R., Zody M.C., Westrov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Searpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope, Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAPTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonCommercial License  
 CC

DR EMBL; CAAB0105006; CAG09535.1; -; Genomic\_DNA.  
 DR InterPro; IPR004043; LCCL.  
 DR InterPro; IPR002035; WVF\_A.  
 DR Pfam; PF03815; LCCL; 1.  
 DR Pfam; PF00092; WVF; 2.  
 DR PRINTS; PR00453; WVFADOMAIN.  
 DR SMART; SM00603; LCCL; 1.  
 DR SMART; SM00327; VMA; 2.  
 DR PROSITE; PS50820; LCCL; 1.  
 DR PROSITE; PS50234; WMPA; 2.  
 FT NON TER 1  
 SQ SEQUENCE 680 AA; 74841 MW; E6B866AF3A17C1A6 CRC64;

Query Match 55.1%; Score 1929; DB 2; Length 680;  
 Best Local Similarity 56.5%; Pred. No. 8.9e-117;  
 Matches 393; Conservative 88; Mismatches 145; Indels 70; Gaps 10;

QY 37 PKFTVQINDVYAKGIIDPEFIKVPACQDPRHYGVDVYASVCGAAVHSGVLD 96  
 DB 1 PSAVIPAIEDVYAKGINIDPEFIKVPACQDPRHYGVDVYASVCGAAVHSGVIT 60  
 QY 97 NSGKILVRYAGOSGKYSNGVOSLSPRRRESFVLESKPKKGVTPSALTYSSSK 156  
 DB 61 NSGKILVRYAGOSGKYSNGVOSLSPRRRESFVLESKPKKGVTPSALTYSSSK 120  
 QY 157 SPAQAGET-TKAYQRPPIPGTTAOPVITLMQLAVTAVATPTTLR-----RPSPSAAS 209  
 DB 121 PTYVKTSETRELVY-----IQXDAKSLAAVTRTLPMLLVQVGSKLVAK 165  
 QY 210 TTSIPRQSVGHNSQEMDLMSTATYTS-----Q 238  
 DB 166 EVVPAKAPLSDGNLHLLDQVSYSLYTHHTLHTRSKNPGRKRFEGSGGERGLPVRRPGQ 225  
 QY 239 NRPRADPGIQRQDPSGAAPQKPVGADV-----SLGLVPKEELSTOSLEPVS 285  
 DB 226 QRYVSGAATGMDQIIP-GCVFAFSQKGLGSPFVPRSPPTSSISFIFLQKQPAASSLSLRA 284  
 QY 286 GDP-NCKIDISFLIDSTSIKRRFRIOQLADVAQALDIGPAGILMGVQYGNPDATH 344

```

Db      285 DHAECKIDLVFLMDGWSIGKRFKIQKDFLAENQAIVNGPTGPMGVQGDDEPTE 344
Qy      345 FINKTHNSRDLKTAIEKITQROGLSNVGRALISVTNFKPSKANGNSGAPNVVYVWVDG 404
Db      345 ISLSVSSSEARSAVEKITQKGLSHVGRALSTINKQYFSDAANGNAAPNVAVLVLDG 404
Qy      405 WPTDKVEASRLARESGINIFITIEGAANEKQYVVEPNFANKAVCRGTGFSYLHVQSW 464
Db      405 WPTDKVEASRLARESGINIFITIEGPDGLEKQVVEHDPVDAVCRGTGFSFLPSSW 464
Qy      465 FGLHKLQPLVKRYCDTRLACSTCINSADIGFVIDGSSSVGTGNFRVYLQFVNTLTK 524
Db      465 FARKLVQPLVKRYCDTRLVCSCTCINANDIAFVIDGSSSVGTGNFRVYLQFVANTIRE 524
Qy      525 FEISDTRIGAVOYTYEORLEFGFDKYSKPDILNAIKRYVSGSTGTAINFALQ 584
Db      525 FEISDTRIGAVOYTYEORLEFSGYQKADLGLAIKRTSWSGSTGTAINFALQ 584
Qy      585 LFKSKENKRLMLITDGRSYDDVRIPMAAHLKGVITYAI--GVMAAQBELVIATH 642
Db      585 LFKSKENKRLMLITDGRSYDDVRIPMAAHLKGVITYAI--GVMAAQBELVIATH 642
Qy      643 PARDHSEFVDFPNLHQYVPRITONICTENSOPRN 678
Db      643 PARDHSEFVDFPNLHQYVPRITONICTENSOPRN 678
Qy      645 PDAHSEFVDFPNLHYKFPRIVSNICOFENSOFRN 680
Db      645 PDAHSEFVDFPNLHYKFPRIVSNICOFENSOFRN 680

```

## RESULT 12

```

Q8AN56_BRARE PRELIMINARY; PRT; 553 AA.
AC 08AN56;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE Novel protein similar to human coagulation factor C homolog (Cochlin,
DE COCH).
GN Name=Coch; Synonyms=OTTARP0000001491; ORFNames=d2234G15.4-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RA Babbage A.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
-----
DR EMBL; AL596026; CAD58748.1; -; Genomic_DNA.
DR HSSP; 043405; 1JBI.
DR Ensembl; ENSDARG00000024032; Danio rerio.
DR ZFIN; ZDB-GENE-030616-403; coch.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VMA; 2.
SQ SEQUENCE 553 AA; 60351 MW; 4A3B136747C488F0 CRC64;

```

```

Query Match 33.9%; Score 1187.5; DB 2; Length 553;
Best Local Similarity 37.7%; Pred. No. 1,3e-68;
Matches 251; Conservative 107; Mismatches 184; Indels 123; Gaps 8;
Qy 16 FLVLVLVGVHS---NKETAKKIRPKFTVPOQIKCDVAKAGIIDPEFIVCPAGCCDPKY 71
Db 5 FAVLHLVGLISLWSCTSGSELNVATP-----ISGTRAVDLSDTHLLVCPANGSLWSL 58

```

```

Qy      72 HVYGTDVASYSYSSVCGAAVHSGVLNDSGKILVRKAVAGOSGYSGYSNGVOSLSLPRMRE 121
Db      59 SVYSGGVASISSICGAATHRGITIGLSGPEVHNGQGRNTNLSYAHAGVQSSLSQWSA 118
Qy      132 SFTVLESKPKKGVTPSALTYSSSKSPAQAQETTYAQRPIPGTTAQPVTLMQLAVT 191
Db      119 SF-----
Qy      192 VAVATPTTLPRPSPAASSTSIIPRQSVGHRSGEMDLMSTATYTSSQNPRAADPGIQRD 251
Db      121 -TVARTISLPLEVSSQTSSTSAIV-----
Qy      252 PSGAARQKPVGADVSLGLVKEELSTQSLPVSAGDPNCKIDLSFLIDSTSIGKRFR 311
Db      143 ASGAA-KKPVK-----IVK-----PPPTAHKDCQVDWALLDSSVYNGRRFNL 188
Qy      312 QKQLADVAQALDIGAGPLMVYQGDNPATFENLKTHTNSDLKTAIEKITQROGLSN 371
Db      189 QKNFVKLATMLKVGTQGPVHVQTSPTPRPFYLTNTYTTADVFAIKEIPIYGANTN 248
Qy      372 VGRATFVTKNFPSKANGRSGAPNVVYVWDGMPDKVEASRLARESGINIFITIEG 431
Db      249 TGRALHTVRNFPSPDFVRRGYPRIYVVFVDSGMPDNEBAAILARESGINIFVSVAK 308
Qy      432 AAENEKQYVVEPNFANKAVCRGTGFSYLHVQSWFGLHKLQPLVKRYCDTRLACSKTCL 491
Db      309 PSPBEASIVSDQPMKRAVCKDNEFFTFMPGSMFSTNKKVPLAQGLCSIDQLGSKTCV 368
Qy      492 NSADIGFVIDGSSSVGTGNFRVYLQFVNTLTKFEISDTRIGAVOYTYEORLEFGFDK 551
Db      369 NSVDLGFLLDGSSSVSDGNFRVLDDLVIARSFSDIGSRGAIQFTYDQMEPNFND 428
Qy      552 YSKSPDILNAIKRYVSGSTGTAINFALBELFKSKYPNKRKMLITDGRSYDDVR 611
Db      429 HUKDVALRLQKIPMSGRTATGDALNFAVNSLFRPSSNRKFLIITDGRSYDDVR 488
Qy      612 PMAAHLKGVITYAIGVMAAQBELVIATHPARDSFVDEPNLHQYVPRITONIC-- 669
Db      489 PMAAAGREGITYAVGVMAAPMEDLKAMASEPKESHVFTREPTGIGRQGPVIRGICRD 548
Qy      670 -TEFN 673
Db      549 FTEFN 553

```

## RESULT 13

```

ID COCH_CHICK STANDARD; PRT; 547 AA.
AC 042163;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 39.
DE Cochlin precursor (COCH-SB2).
GN Name=COCH; Synonyms=COCHSB2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN 1;
RP NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND DEVELOPMENTAL
RP STAGE.
RC STRAIN=White leghorn; TISSUE=Baellar papilla;
RX MEDLINE=98409669; Pubmed=9736748; DOI=10.1073/pnas.95.19.11400;
RA Heller S., Sheane C.A., Javed Z., Hudepeth A.J.;
RT "Molecular markers for cell types of the inner ear and candidate genes
RT for hearing disorders.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11400-11405(1998).
CC -!- SUBCELLULAR LOCATION: Secreted protein (potential).
CC -!- TISSUE SPECIFICITY: Expressed in inner ear structures: the
CC spindle-shaped cells of the basilar papilla, weaker expression
CC found in the inferior and superior fibrocyticlaginous plates and

```

```

CC skeletal muscle.
CC -1- DEVELOPMENTAL STAGE: Specifically expressed at the late
CC developmental stages in the cochlea.
CC -1- SIMILARITY: Contains 1 LCCU domain.
CC -1- SIMILARITY: Contains 2 WFA domains.
CC -1- DATABASE: NAME=Protein Spotlight; NOTE=Issue 4 of November 2000;
CC WWW="http://www.expasy.org/spotlight/back_issues/spl004.shtml".
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC
DR EMBL: AF012252; AAC62253.1; -. mRNA.
DR HSSP: O43405; IJBI.
DR Ensembl: ENSGALG0000009920; Gallus gallus.
DR InterPro: IPR004043; LCCU.
DR InterPro: IPR002035; WFA_A.
DR Pfam: PF03815; LCCU; 1.
DR Pfam: PF00092; WFA; 2.
DR PRINTS: PR00453; WFADOMAIN.
DR SMART: SM00603; LCCU; 1.
DR SMART: SM00327; WFA; 2.
DR PROSITE: PS00820; LCCU; 1.
DR PROSITE: PS00334; WFA; 2.
DR GlycoProtein: Repeat; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 1 547 Cochlin.
FT FTID=PRO_0000020967.
FT DOMAIN 24 117 LCCU.
FT DOMAIN 162 347 WFA 1.
FT DOMAIN 364 534 WFA 2.
FT CARBHD 218 218 N-linked (GlcNAc...) (Potential).
FT DISULFID 30 46 By similarity.
FT DISULFID 70 70 By similarity.
SQ SEQUENCE 547 AA; 59427 MW; 172724242641DF88 CRC64;

Query Match 32.5%; Score 1139; DB 1; Length 547;
Best Local Similarity 37.3%; Pred. NO. 1.9e-65;
Matches 229; Conservative 104; Mismatches 165; Indels 116; Gaps 5;

QY 60 VKCPAGCDDPKYHVTGTVASYSVCGAAHVGVLDSGGKILRVKVAAGSGKSGSYN 119
DB 44 VLPKANCNLMQFYFGDVIYSLSSVCGAAHHRGVTNAGAAVQVLPQGENPANHAN 103
QY 120 GVQSLSPRWRSEFVLESKRKGVTPSALTYSKSPAAQAGRTTAYORPPITGTTA 179
DB 104 GIGCVFGRWMSSEFV-----TPGTNN 125
QY 180 QPVLMLQALVAVATPTTIPRSPASATSTIPRQSVGHRQENDLMSTATTYSQN 239
DB 126 ---LAEVGRSVATARPAT----- 142
QY 240 RPRADPGIQRDPGGAFOKPVGADVSLGLVPEKESTOSLEPVSLGDPNCKIDSLFID 299
DB 143 -----GKPKTKLEKA-----GNKDKADIAFLID 168
QY 300 GSTSIGKRRFRIQKQLADVAQALDIGPAGLGMVQYGDPAFTHFNLTHTNSRDLTXA 359
DB 229 IKELGFRGNSNTKALHGAQKFFSMENGRKGI PKLIIVFLDGWPSDDLEBGIVARE 288
QY 169 GSYNIGGRFNLQKNFVGKAVVLMGIGTEGPHVGVQASEHPKLEFYLNKTAKEVLA 228
QY 360 IEXTTGGLSNVGRALSFVTKNFFSKANGRSAPNVVVVMDGMPDKKEEKLARE 419
DB 229 IKELGFRGNSNTKALHGAQKFFSMENGRKGI PKLIIVFLDGWPSDDLEBGIVARE 288
QY 420 SGINIFFTIGGAENEKQYVVEPFAKAVCRITNGFSLHVOSEFGHLKTLQPLVAVK 479
DB 289 FGVAVFIVAKPTTEELGMVODIGFIDKAVCRNNGFSSYQMPSPFGTTKYKFLVQKLC 348
QY 480 DTDLACSKTCLNSADIGFVIDSSSVGTGNFVTLQFVTLKFEISDTRIGAVQY 539
DB 349 SHEQMLCSKTCYNVSNIGFLIDSSSVGSNFRILMLEPISVAVAKAFEISDGIATVQF 408
QY 540 TYEGRLGEPDKYSKSDILNAIKRVGVWGGTGTGAINALQLPFGKSPNKR-LMI 598

```

```

DB 409 TYDQRTSFSDYTTKERVLSAIRNIRYMSGATGDAISFTTNRVGPVKANKFLV 468
QY 599 LITGRSYDPRIPAMAHLKGVITVAIGVAAQEELEVATAPARDHSFVDFDLH 658
DB 469 LITGCGSYDVRGAVAAQKRGITVPSGVAAAPLDLKKMASPRESHFTTFEFGLE 528
QY 659 QYVPRIIQNTCTEF 672
DB 529 QMVDVIRGICKDF 542

RESULT 14
COCH_HUMAN
ID COCH_HUMAN STANDARD; PRT; 550 AA.
AC O43405;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 56.
DE Cochlin precursor (COCH-5B2).
GN Name=COCH; Synonyms=COCH5B2; ORFNames=UNQ257/PRO294;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Cochlea;
RX MEDLINE=98110569; PubMed=9441737; DOI=10.1006/geno.1997.5067;
RA Robertson N.G., Skvorak A.B., Yin Y., Weremowicz S., Johnson K.R.,
RA Kovatch K.A., Battey J.F., Bieber F.R., Morton C.C.;
RT "Mapping and characterization of a novel cochlear gene in human and in
RL mouse: a positional candidate gene for a deafness disorder, DFNA9.";
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chan J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Bacon D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Kimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagtes A.,
RA Vanden R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yasuna D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ARG-135; ASN-281;
RP SER-352 AND VAL-402.
RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Bettucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
RT "SeattleSNPs, NHLBI H66682 program for genomic applications, UW-
RT PHRC, Seattle, WA (URL: http://pga.gs.washington.edu)";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP N-GLYCOSYLATION, SUBCELLULAR LOCATION, AND PROTEOLYTIC PROCESSING.
RX MEDLINE=22727166; PubMed=12843317; DOI=10.1136/jmg.40.7.479;
RA Robertson N.G., Hamaker S.A., Patriub V., Aster J.C., Morton C.C.;
RT "Subcellular localization, secretion, and post-translational
RT processing of normal cochlin, and of mutants causing the sensorineural
RT deafness and vestibular disorder, DFNA9.";
RL J. Med. Genet. 40:479-486(2003).
RN [5]
RP STRUCTURE BY NMR OF 27-126.
RX MEDLINE=21458424; PubMed=11574466; DOI=10.1093/emboj/20.19.5347;
RA Ljepush E., Tsexler M., Kalkonen A., Weigelt J., Banyai L.,
RA Patthy L., Oetting G.,
RT "NMR structure of the LCCU domain and implications for DFNA9 deafness
RT disorder.";

```

EMBO J. 20:5347-5353 (2001).  
[6]  
VARIANTS DFNA9 GLY-66; GLU-88 AND ARG-117.  
RX MEDLINE=99021390; PubMed=9806553; DOI=10.1038/3118;  
RA Robertson N.G., Lu L., Haller S., Merchant S.N., Baye R.D.,  
RA McGenna M., Nadol J.B. Jr., Miyamoto R.T., Linthicum F.H. Jr.,  
RA Neco J.F.L., Hudspeth A.J., Seidman C.E., Morton C.C., Seidman J.G.;  
RT "Mutations in a novel cochlear gene cause DFNA9, a human nonsyndromic  
RT deafness with vestibular dysfunction.";  
RL Nat. Genet. 20:299-303 (1998).  
[7]  
VARIANT DFNA9 SER-51.  
RX MEDLINE=99155917; PubMed=9931344; DOI=10.1093/hmg/8.2.361;  
RA de Kok Y.J.M., Bom S.J.H., Brunt T.M., Kemperman M.H.,  
RA van Beuskom E., van der Velde-Vissers S.D., Robertson N.G.,  
RA Morton C.C., Huygen P.L.M., Verhagen W.I.M., Brunner H.G.,  
RA Cremers C.W.R.J., Cremers F.P.M.;  
RT "A Pro51ser mutation in the COCH gene is associated with late onset  
RT autosomal dominant progressive sensorineural hearing loss with  
RT vestibular defects.";  
RL Hum. Mol. Genet. 8:361-366 (1999).  
[8]  
VARIANT DFNA9 SER-51.  
RX MEDLINE=99330549; PubMed=10400989; DOI=10.1093/hmg/8.8.1425;  
RA Franssen E., Verstrecken M., Verhagen W.I.M., Wuyts F.L., Huygen P.L.M.,  
RA D'Haese P., Robertson N.G., Morton C.C., McGuffit W.T., Smith R.J.H.,  
RA Declau F., Van de Heyning P.H., Van Camp G.;  
RT "High prevalence of symptoms of Meniere's disease in three families  
RT with a mutation in the COCH gene.";  
RL Hum. Mol. Genet. 8:1425-1429 (1999).  
[9]  
VARIANT DFNA9 ASN-109.  
RX MEDLINE=91193177; PubMed=11295836; DOI=10.1002/humu.37;  
RA Kaminaros M., McGill J., Lynch M., Dahl H.-H.M.;  
RT "Identification of a novel COCH mutation, I109N, highlights the  
RT similar clinical features observed in DFNA9 families.";  
RL Hum. Mutat. 17:351-351 (2001).  
[10]  
ERRATUM.  
RA Kaminaros M., McGill J., Lynch M., Dahl H.-H.M.;  
RL Hum. Mutat. 18:547-548 (2001).  
[11]  
VARIANT DFNA9 THR-119.  
RX MEDLINE=22873884; PubMed=14512963; DOI=10.1038/sj.ejhg.5201043;  
RA Usami S., Takahashi K., Yuge I., Ohtsuka A., Namba A., Abe S.,  
RA Franssen E., Patchy L., Oetting G., Van Camp G.;  
RT "Mutations in the COCH gene are a frequent cause of autosomal dominant  
RT progressive cochleo-vestibular dysfunction, but not of Meniere's  
RT disease.";  
RL Eur. J. Hum. Genet. 11:744-748 (2003).  
[12]  
CHARACTERIZATION OF VARIANTS DFNA9 SER-51; GLY-66; GLU-88; ASN-109 AND  
RP ARG-117.  
RX MEDLINE=22866966; PubMed=12928864; DOI=10.1007/s00439-003-0992-7;  
RA Grabatski R., Szul T., Sasaki T., Timpl R., Wayne R., Hicks B.,  
RA Szul E.;  
RT "Mutations in COCH that result in non-syndromic autosomal dominant  
RT deafness (DFNA9) affect matrix deposition of cochlin.";  
RL Hum. Genet. 113:406-416 (2003).  
[13]  
DISEASE.  
RX MEDLINE=21453839; PubMed=11568667;  
RX DOI=10.1097/00129492-200109000-00009;  
RA Boulassel M.-R., Tomasi J.-P., Deggouj N., Gerardoff M.;  
RT "COCHB2 is a target antigen of anti-inner ear antibodies in  
RT autoimmune inner ear diseases.";  
RL Otol. Neurotol. 22:614-618 (2001).  
-1- SUBCELLULAR LOCATION: Secreted protein; extracellular space;  
-1- TISSUE SPECIFICITY: Expressed in inner ear structures; the cochlea  
-1- and the vestibule.  
-1- PTM: N-glycosylated.  
-1- PTM: A 50 kDa form is created by proteolytic cleavage.

CC	-1-	DISEASE: Defects in COCH are the cause of autosomal dominant nonsyndromic sensorineural deafness type 9 (DFNA9) [MIM:603369].
CC		Hearing loss begins in the fourth or fifth decade of life and initially involves the high frequencies. Deafness is progressive and usually complete by the sixth decade. In addition to cochlear involvement, DFNA9 patients also exhibit a spectrum of vestibular dysfunctions. Penetrance of the vestibular symptoms is often incomplete, and some patients are minimally affected, whereas others suffer from severe balance disturbances and episodes of vertigo. Affected individuals have mucopolysaccharide depositions in the channels of the cochlear and vestibular nerves. These depositions apparently cause strangulation and degeneration of dendritic fibers.
CC	-1-	DISEASE: Defects in COCH may contribute to Meniere disease [MIM:156000]. Meniere disease is an autosomal dominant disorder characterized by hearing loss associated with episodic vertigo. Antibodies against the protein COCH are found in 10% of Meniere patients.
CC	-1-	SIMILARITY: Contains 1 LCCL domain.
CC	-1-	SIMILARITY: Contains 2 VWFA domains.
CC	-1-	DATABASE: NAME=Protein Spotlight; NOTE=Issue 4 of November 2000; WWW="http://www.expasy.org/spotlight/back_issues/split004.shtml".
CC	-1-	DATABASE: NAME=Hereditary hearing loss homepage; NOTE=Gene page; WWW="http://webhost.ua.ac.be/hhh/".
CC		-----
CC		Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
CC		Distributed under the Creative Commons Attribution-NoDerivs License
CC		-----
DR	EMBL	AF006740; AAC39545.1; -; mRNA.
DR	EMBL	AY358900; AA089259.1; -; mRNA.
DR	EMBL	AY916789; AAM82432.1; -; Genomic_DNA.
DR	PDB	1UBI; NMR; A=28-124.
DR	Ensembl	ENSG00000100473; Homo sapiens.
DR	HGNC	HGNC:2180; COCH.
DR	MIM	156000; phenotype.
DR	MIM	603369; phenotype.
DR	MIM	603196; gene.
DR	GO	GO:0007605; P:perception of sound; TAS.
DR	InterPro	IPR004043; LCCL.
DR	InterPro	IPR002035; VWF_A.
DR	Pfam	PF03815; LCCL, 1.
DR	Pfam	PF00092; VWF, 2.
DR	PRINTS	PR00453; VWFADOMAIN.
DR	SMART	SM00603; LCCL, 1.
DR	SMART	SM00327; VWF, 2.
DR	PROSITE	PS50820; LCCL, 1.
DR	PROSITE	PS50234; VWFA, 2.
KW	3D-structure	Deafness; Disease mutation; Glycoprotein; Polymorphism;
KW	Repeat	Signal.
KW	SIGNAL	1
FT	CHAIN	25 550 Potential.
FT		Cochlin.
FT		/Frid=PRO_000020968.
FT	DOMAIN	28 121 LCCL.
FT	DOMAIN	165 346 VWFA 1.
FT	DOMAIN	367 537 VWFA 2.
FT	CARBOHYD	100 100 N-linked (GlcNAc . .) (Potential).
FT	CARBOHYD	221 221 N-linked (GlcNAc . .) (Potential).
FT	DISULFID	34 50
FT	DISULFID	54 74
FT	VARIANT	51 51
FT		P -> S (in DFNA9; Meniere disease; does not affect protein deposition to the extracellular matrix).
FT		extracellular matrix.
FT		/Frid=VAR_008532.
FT	VARIANT	66 66 V -> G (in DFNA9; affects protein deposition to the extracellular matrix).
FT		/Frid=VAR_008533.
FT	VARIANT	88 88 G -> E (in DFNA9; affects protein deposition to the extracellular matrix).
FT		
Query Match		32.3%; DB 1; Length 550;
Best Local Similarity		37.1%; Pred. No. 7,86-65;
Matches 234,	Conservative 103;	Mismatches 175; Indels 119; Gaps 7;

```

Db      | 32 ITCTFRGLDIRKEKADVLCPGGCPLEEFSSVGNIVYASVSSICGAARGVATNSGGGVR 91
Qy      | 104 VRKVGOSGYKGSYNSGVOSLSLPRMRESFVLESKPKKGVTPALTYSSSKSPAQAQ 163
Db      | 92 VYSLGRENYSVDNANGIOSQMLSRMSASFVYTKK-----SQTQATGA- 137
Qy      | 164 ETTKAYQRPPIPGTTAQPVTLMQLLAVTAVATPTTLPRSPSAASTTSIPRPOSVGHR 223
Db      | 138 -----VSTAHF----- 143
Qy      | 224 QEMDLMSTATYTSSQNRPRADPGIORODPSGAAPKPGADVSLGLVPEKELSTQSLPV 283
Db      | 144 -----PTGRRLK-----TPEKK----- 156
Qy      | 284 SLGPNCKIDLFLIDGSTSGKRRFRIOKOLLADVAOALDIGPAPLMGVQGDNPAT 343
Db      | 157 -TGNDCKADIAFLIDGSFNIGORFNLQKNFVGVALMLGIGTEGPHVGLVQASHPKI 215
Qy      | 344 HFNKHTNSBDLKTALIEKITORGGLSNVGRASIFVTNPFPSKANGSGAPNVVVVMD 403
Db      | 216 EFLYLNFTSAKVDLFAIKVEVFRGNSNTGKALKHTAQKFVTVAGVAKGIPKVVVFID 275
Qy      | 404 GMPDVKVEASRLARESGINIFITIEGAENKQYVVEPNPANKAVCTRTGFSYLVQS 463
Db      | 276 GMPSDIDEEAGIVAREFGVNFIVSAKPIBELGMQDVTFVDKACVRNNGFFSYHMPN 335
Qy      | 464 WFGHLKTLQPLVKRCVCTDRLACSKTCLNSADIGFVIDSSVGNFRTPLOFNTLTK 523
Db      | 336 WFGTTKYKPLVQKLTCHQEMCMCKTCYNVNIAPFLIDSSSVGDSNFRMLMEFVSNIAK 395
Qy      | 524 EPEISDTRIGAVQYTYEORLEFGFDKYSKPDILNAIKVGVSGSTGTAINFAL 583
Db      | 396 TFEISDIGAKIAAVQFYDQRTFESFTDYSTEKNVLAVIRNIRVMSGTATGDAISFTVR 455
Qy      | 584 QLFK--KSKPKRKMILITDGRSYDVRIPMAAHLKGVITTAIGVAAAQOELEVIAT 641
Db      | 456 NVFGPIRSPNK-NFLVITVDGOSYDDVQGPAAAHADAGITIFSVGAMAPLDLCKMAS 514
Qy      | 642 HPARDHSFVDEFDNLHQVPRIIIONICTEF 672
Db      | 515 KPKEASHAFTRFETGLEPIVSDVIRGICRDF 545

RESULT 15
OSEA64_BOVIN PRELIMINARY; PRT; 550 AA.
ID OSEA64_BOVIN
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2006, entry version 1.
DE Coagulation factor C homolog, cochl.
GN Name=COCH;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Poolled.
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Casas E., Wray J.E., White J., Cho J., Fehrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-Mckom C.G.,
RA Petrea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keefe J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RL 1 libraries and construction of a gene index for cattle.";
RN Genome Res. 11:626-630(2001).
RP [2]
RC TISSUE=Poolled.

```

```

RA Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keefe J.W.,
RA Snelling W.M., Weidman R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC
DR EMBL; BT020705; AA08722.1; -; mRNA.
DR SMR; OSEA64; 29-124.
DR Ensemble; ENSBTAG00000021844; Bos taurus.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF03815; LCCL.1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL.1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL.1.
DR PROSITE; PS50234; VWF_A; 2.
SQ SEQUENCE 550 AA; 59594 MW; DB3B21839C68D209 CRC64;

Query Match 32.1%; Score 1123.5; DB 2; Length 550;
Best Local Similarity 36.8%; Pred. No. 1.9e-64;
Matches 232; Conservative 103; Mismatches 177; Indels 119; Gaps 7;

Qy 44 INCVKKKGIIDPEFIKVCAGCDDPKYHYGTDVYASVSGVGAHSGVLDNGGKIL 103
Db 32 ITCTFRGLDIRKEADVLCPGGCPLEEFSSVGNIVYASVSSICGAARGVATNSGGGVR 91
Qy 104 VRKVGOSGYKGSYNSGVOSLSLPRMRESFVLESKPKKGVTPALTYSSSKSPAQAQ 163
Db 92 VYSLGRENYSVDNANGIOSQMLSRMSASFVYTKK-----SQTQATGA- 137
Qy 164 ETTKAYQRPPIPGTTAQPVTLMQLLAVTAVATPTTLPRSPSAASTTSIPRPOSVGHR 223
Db 138 -----VSTAHF----- 148
Qy 224 QEMDLMSTATYTSSQNRPRADPGIORODPSGAAPKPGADVSLGLVPEKELSTQSLPV 283
Db 149 -----LKTPEKK----- 156
Qy 284 SLGPNCKIDLFLIDGSTSGKRRFRIOKOLLADVAOALDIGPAPLMGVQGDNPAT 343
Db 157 -TGNDCKADIAFLIDGSFNIGORFNLQKNFVGVALMLGIGTEGPHVGLVQASHPKI 215
Qy 344 HFNKHTNSBDLKTALIEKITORGGLSNVGRASIFVTNPFPSKANGSGAPNVVVVMD 403
Db 216 EFLYLNFTSAKVDLFAIKVEVFRGNSNTGKALKHTAQKFVTVAGVAKGIPKVVVFID 275
Qy 404 GMPDVKVEASRLARESGINIFITIEGAENKQYVVEPNPANKAVCTRTGFSYLVQS 463
Db 276 GMPSDIDEEAGIVAREFGVNFIVSAKPIBELGMQDVTFVDKACVRNNGFFSYHMPN 335
Qy 464 WFGHLKTLQPLVKRCVCTDRLACSKTCLNSADIGFVIDSSVGNFRTPLOFNTLTK 523
Db 336 WFGTTKYKPLVQKLTCHQEMCMCKTCYNVNIAPFLIDSSSVGDSNFRMLMEFVSNIAK 395
Qy 524 EPEISDTRIGAVQYTYEORLEFGFDKYSKPDILNAIKVGVSGSTGTAINFAL 583
Db 396 TFEISDIGAKIAAVQFYDQRTFESFTDYSTEKNVLAVIRNIRVMSGTATGDAISFTVR 455
Qy 584 QLFK--KSKPKRKMILITDGRSYDVRIPMAAHLKGVITTAIGVAAAQOELEVIAT 641
Db 456 NVFGPIRSPNK-NFLVITVDGOSYDDVQGPAAAHADAGITIFSVGAMAPLDLCKMAS 514
Qy 642 HPARDHSFVDEFDNLHQVPRIIIONICTEF 672
Db 515 KPKEASHAFTRFETGLEPIVSDVIRGICRDF 545

Search completed: September 5, 2006, 20:07:20

```

Wed Sep 6 10:42:03 2006

us-10-063-538-34.rup.spd1

Page 26

Job time : 370 secs

---



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

## OM protein - protein search, using sw model

Run on: September 5, 2006, 19:59:38 ; Search time 44 Seconds

(without alignments)  
1482.613 Million cell updates/sec

Title: US-10-063-538-34

Perfect score: 3502

Sequence: 1 MRTVLTMKASVEMFLVL.....QYVPRIIQICTERNQPRN 678

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : pIR\_80:\*

1: pIR1:\*

2: pIR2:\*

3: pIR3:\*

4: pIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	15.8	3124	2 A40020	collagen alpha 1(X
2	504.5	14.4	3137	2 A37797	collagen alpha 3(V
3	501.5	14.3	496	2 A37979	cartilage matrix p
4	490	14.0	493	2 A33809	cartilage matrix p
5	490	14.0	500	2 S65522	cartilage matrix p
6	471.5	13.5	3176	2 CGH03A	collagen alpha 3(V
7	331	9.5	1857	2 S31212	collagen alpha 1(X
8	331	9.5	1888	2 S78476	collagen alpha 1(X
9	329.5	9.4	2944	2 A54849	collagen alpha 1(X
10	329	9.4	1747	2 A45974	collagen alpha 1(X
11	314.5	9.0	567	2 T28797	collagen alpha 1(X
12	298	8.5	741	2 T46488	hypothetical prote
13	280.5	8.0	929	2 I51027	type XII collagen
14	279	8.0	3051	2 S42373	hypothetical prote
15	266	7.6	2813	1 VMHU	von Willebrand fac
16	262.5	7.5	843	2 A40970	undulin 1 - human
17	252.5	7.2	1019	1 A32856	collagen alpha 1(V
18	231	6.6	1153	1 RMHUIB	cell surface glyco
19	229	6.5	550	2 T23760	hypothetical prote
20	229	6.5	1153	2 S00551	leukocyte surface
21	228	6.5	1163	1 RMHUIC	cell surface glyco
22	226.5	6.5	427	2 G00039	von Willebrand fac
23	226.5	6.5	1025	2 S34833	collagen alpha 1(V
24	213.5	6.1	414	2 P50323	von Willebrand fac
25	213.5	6.1	1286	2 A68396	protein M01E0.2 f
26	210.5	6.0	2098	2 T18397	protein CTRP - mal
27	209.5	6.0	1022	2 S04111	collagen alpha 2(V
28	209	6.0	918	2 S23377	collagen alpha 2(V
29	205	5.9	1028	1 CGH01A	collagen alpha 1(V

30	205	5.9	1029	1 S21369	collagen alpha 2(V
31	204	5.8	11055	2 T16580	hypothetical prote
32	203.5	5.8	1170	2 S03308	cell surface glyco
33	203.5	5.8	1180	2 A35854	integrin alpha-1 c
34	200	5.7	238	2 C35243	collagen alpha 2(V
35	200	5.7	917	2 S09646	collagen alpha 2(V
36	200	5.7	1018	1 CGH02A	collagen alpha 2(V
37	195	5.6	1163	2 S6126	lymphocyte fuction
38	193	5.5	1151	2 A45226	integrin alpha-1 c
39	188.5	5.4	272	2 A55348	integrin alpha-1 c
40	187.5	5.4	1170	2 T45914	integrin alpha 2 s
41	184.5	5.3	643	2 T19549	hypothetical prote
42	182.5	5.2	1181	2 A33958	integrin alpha-2 c
43	178	5.1	763	2 T50807	complement factor
44	171	4.9	712	2 A45638	immunodominant mic
45	170.5	4.9	1178	2 S44142	VIA-2 protein homo
46	166.5	4.8	191	2 T47230	VIA-2 protein - pi
47	162.5	4.6	1179	2 A53213	integrin alpha-B c
48	159.5	4.6	1019	2 A38738	coagulation factor
49	159	4.5	640	2 T29784	hypothetical prote
50	150.5	4.3	724	2 A48569	antigen Em100 - Ei
51	146	4.2	371	2 S32604	collagen alpha 2(V
52	141.5	4.0	2938	2 T30249	cell proliferation
53	140.5	4.0	449	2 T33257	hypothetical prote
54	135.5	3.9	833	2 AF2089	hypothetical prote
55	131	3.7	959	2 S32605	collagen alpha 3(V
56	128.5	3.7	341	2 T32949	hypothetical prote
57	128	3.7	1200	2 T17404	hyalin - sea urchi
58	125.5	3.6	474	2 T31064	hypothetical prote
59	125.5	3.6	661	2 T16587	hypothetical prote
60	125	3.6	478	2 T10030	hypothetical prote
61	125	3.6	586	2 H86914	conserved hypotet
62	124.5	3.6	921	2 G02326	transcription fact
63	123.5	3.5	460	2 T23087	hypothetical prote
64	122.5	3.5	1777	2 T34369	hypothetical prote
65	122	3.5	1595	2 T31082	endo-1,4-beta-xyla
66	121.5	3.5	445	2 B40970	undulin 2 - human
67	121.5	3.5	915	2 T09575	smoothenin - human
68	120.5	3.4	2013	2 AD1129	probable peptidogl
69	120	3.4	573	2 A33533	cell surface glyco
70	120	3.4	939	2 AE2275	hypothetical prote
71	119	3.4	725	2 A4258	hypothetical prote
72	119	3.4	1328	2 T43060	agrin - electric r
73	119	3.4	1588	2 A46036	probable adhesin Z
74	119	3.4	1588	2 H91188	cadherin-7 - chick
75	118.5	3.4	785	2 T50180	von Willebrand fac
76	117.5	3.4	780	2 A34102	genome polyprotein
77	116	3.3	2733	2 S15760	threonine ammonia-
78	115	3.3	595	2 A38628	hypothetical prote
79	114	3.3	227	2 T12549	p45 NF-E2 related
80	114	3.3	581	2 T49261	glycerophosphoryl
81	114	3.3	786	2 D75630	Lu-ECM-1 protein
82	114	3.3	905	2 T02205	related to suppres
83	114	3.3	1174	2 T49688	hypothetical prote
84	113	3.2	771	2 T34376	transforming prote
85	112.5	3.2	428	1 TVHUEK	signal recognition
86	112.5	3.2	638	2 A24570	hypothetical prote
87	112.5	3.2	1028	2 T34360	hypothetical prote
88	112	3.2	484	2 F83330	RND divalent metal
89	112	3.2	710	2 T44753	hypothetical prote
90	112	3.2	733	2 A87168	conserved hypotet
91	112	3.2	1557	2 T13160	protein CNK - fruit
92	112	3.2	1660	2 A84647	hypothetical prote
93	112	3.2	2214	2 T16305	hypothetical prote
94	111.5	3.2	382	2 T14336	hypothetical prote
95	111.5	3.2	385	2 E96669	RAD23 protein, iso
96	110.5	3.2	1066	2 G84746	protein PIN19.19 f
97	110.5	3.2	1081	2 S66736	hypothetical prote
98	110	3.1	853	2 AC2079	transcription acti
99	110	3.1	1367	1 A8478	ferrichrome-iron r
100	109.5	3.1	667	2 T00061	glucan 1,4-alpha-g
101	109.5	3.1	1809	2 S57329	hypothetical prote
102	109	3.1	270	2 E87649	tuberos scleriosis
					hypothetical prote

103	109	3.1	452	2	T46147	176	101.5	2.9	632	2	D98191	trka-like protein
104	109	3.1	802	2	T21315	177	101.5	2.9	881	2	S56032	probable membrane
105	109	3.1	1091	2	S3850	178	101.5	2.9	932	2	T21338	hypothetical prote
106	108.5	3.1	652	2	T37882	179	101.5	2.9	1093	2	I38533	AF17 protein - hum
107	108.5	3.1	1779	2	T31085	180	101.5	2.9	1335	2	T30211	autolysin E - Staph
108	108	3.1	402	1	QRB072	181	101.5	2.9	1943	2	B64596	toxlin-like outer m
109	108	3.1	511	2	I50114	182	101.5	2.9	2166	2	H89960	hypothetical prote
110	108	3.1	1324	2	S52863	183	101	2.9	497	2	T41015	proline rich prote
111	108	3.1	1634	2	T26517	184	101	2.9	932	2	T40216	probable histone t
112	107.5	3.1	509	2	AG0365	185	101	2.9	949	2	JC7802	Urb protein - mous
113	107.5	3.1	1200	2	T48194	186	101	2.9	1927	2	T15243	hypothetical prote
114	107.5	3.1	1501	2	T45623	187	101	2.9	1575	2	S68448	synproctamin, 170k
115	107	3.1	432	2	UC4864	188	101	2.9	3216	2	C90538	hypothetical prote
116	107	3.1	660	2	JM0067	189	100.5	2.9	433	2	S52974	regulatory protein
117	107	3.1	856	2	C85023	190	100.5	2.9	593	2	D97806	penicillin-binding
118	107	3.1	1450	2	C86880	191	100.5	2.9	645	2	G01205	TYL protein - huma
119	106.5	3.0	721	2	T41530	192	100.5	2.9	769	2	T22313	hypothetical prote
120	106.5	3.0	794	2	T37989	193	100.5	2.9	832	2	T31288	hypothetical prote
121	106.5	3.0	800	2	S29344	194	100.5	2.9	878	1	A40091	interleukin-3 rece
122	106	3.0	351	2	S50754	195	100.5	2.9	1220	2	T19117	hypothetical prote
123	106	3.0	691	2	B75622	196	100.5	2.9	1849	2	C41859	IGA-specific metal
124	106	3.0	963	2	T48707	197	100.5	2.9	2354	2	T13288	mei-41 protein - f
125	106	3.0	1072	2	A37127	198	100	2.9	371	2	F70555	hypothetical prote
126	105.5	3.0	528	2	T52092	199	100	2.9	404	2	T14729	betaine-aldehyde d
127	105.5	3.0	817	2	S51342	200	100	2.9	681	2	I78558	hypothetical Brach
128	105.5	3.0	826	2	A45559	201	100	2.9	718	2	F64628	flagellar hook pro
129	105.5	3.0	1043	2	F97302	202	100	2.9	802	2	B43735	bcsB protein - Ace
130	105.5	3.0	1299	2	T47182	203	100	2.9	873	2	A47283	calphostin - fruit
131	105.5	3.0	1748	1	J01555	204	100	2.9	1006	2	T00050	hypothetical prote
132	105	3.0	367	2	AG3032	205	100	2.9	1045	2	A29840	serine proteinase
133	105	3.0	412	2	E98253	206	100	2.9	1247	2	T45743	hypothetical prote
134	105	3.0	562	1	HMIV2	207	100	2.9	1420	2	T37781	probable cytokele
135	105	3.0	1048	2	A70592	208	100	2.9	2232	2	T34434	hypothetical prote
136	105	3.0	2514	2	F81045	209	99.5	2.8	318	2	E82493	conserved hypochet
137	105	3.0	3005	2	T08841	210	99.5	2.8	436	2	S48399	hypothetical prote
138	104.5	3.0	671	2	T02504	211	99.5	2.8	633	2	AC3634	noid protein limpo
139	104.5	3.0	764	2	S75407	212	99.5	2.8	743	2	T09173	EH domain protein
140	104.5	3.0	880	2	S60137	213	99.5	2.8	1131	2	T41144	hypothetical seixin
141	104.5	3.0	931	2	T49710	214	99.5	2.8	1162	2	T30194	nuclear protein SA
142	104.5	3.0	963	2	T40290	215	99.5	2.8	1196	2	T14108	SH3-containing pro
143	104.5	3.0	2013	2	A11489	216	99.5	2.8	1306	2	S22624	aggregation protei
144	104	3.0	337	1	DEZMGC	217	99.5	2.8	1723	2	H86557	polymorphic membra
145	104	3.0	429	2	UC4965	218	99.5	2.8	1732	2	E72067	polymorphic membra
146	104	3.0	582	2	A70755	219	99.5	2.8	1732	2	C81601	polymorphic membra
147	104	3.0	1091	2	JH0565	220	99.5	2.8	3570	2	T45025	mucin MUC5B, trach
148	104	3.0	1238	2	T34929	221	99	2.8	616	2	B33586	C4-dicarboxylate t
149	104	3.0	1679	2	T50091	222	99	2.8	620	2	A70525	hypothetical prote
150	104	3.0	1802	2	S69703	223	99	2.8	621	2	D96032	C4-dicarboxylate t
151	103.5	3.0	575	2	T21775	224	99	2.8	632	2	T02627	hypothetical prote
152	103.5	3.0	656	2	AB1843	225	99	2.8	655	2	E81157	cell division prot
153	103.5	3.0	837	2	A57542	226	99	2.8	660	1	VHWMH2	structural protein
154	103	2.9	349	2	T05857	227	99	2.8	718	2	G71888	flagellar hook pro
155	103	2.9	616	2	T68292	228	99	2.8	750	2	T48804	hypothetical prote
156	103	2.9	719	2	S60771	229	99	2.8	751	2	B87391	Tomb-dependent rec
157	103	2.9	803	2	S76106	230	99	2.8	761	1	BBMS	complement factor
158	103	2.9	1566	2	T20058	231	99	2.8	766	2	AS6394	pyocin S3 - Pseudo
159	102.5	2.9	256	2	A60533	232	99	2.8	809	2	H87455	Tomb-dependent rec
160	102.5	2.9	425	2	T18723	233	99	2.8	839	2	F75518	hypothetical prote
161	102.5	2.9	465	2	C70594	234	99	2.8	874	2	JC4930	S-layer protein pr
162	102.5	2.9	889	2	A35679	235	99	2.8	1198	2	B88279	protein C08H9.2 [1
163	102.5	2.9	1054	2	S54473	236	99	2.8	1217	2	T39427	probable myosin I
164	102	2.9	353	2	A41558	237	99	2.8	1283	2	T39174	hypothetical Serin
165	102	2.9	392	2	T04150	238	99	2.8	1591	2	AS5416	invasion-inducing
166	102	2.9	719	2	T33170	239	99	2.8	1704	2	A55426	gingipain R (EC 3.
167	102	2.9	776	2	AB0998	240	99	2.8	1744	1	CAHU	complement C4a pre
168	102	2.9	1008	2	T12532	241	99	2.8	1764	2	T15171	hypothetical prote
169	102	2.9	1341	2	S09579	242	98.5	2.8	252	2	T04739	hypothetical prote
170	102	2.9	2229	2	T16199	243	98.5	2.8	329	2	S17765	major storage prot
171	102	2.9	2441	2	S39161	244	98.5	2.8	564	2	AF2351	serine/threonine k
172	101.5	2.9	328	2	C42756	245	98.5	2.8	654	2	T33044	hypothetical prote
173	101.5	2.9	574	2	F75336	246	98.5	2.8	662	2	I36400	melanoma-associate
174	101.5	2.9	631	2	D95348	247	98.5	2.8	668	2	A41234	melanocyte-specific
175	101.5	2.9	632	2	AF3095	248	98.5	2.8	746	2	T46821	siderophore recep

249	98.5	2.8	746	2	A95420	Rhta Rhizobactin r	322	96.5	2.8	1219	2	T14578	nucleoporin Nup153
250	98.5	2.8	790	2	T47959	hypothetical prote	323	96.5	2.8	1433	2	A71444	probable LTR retro
251	98.5	2.8	970	2	F87450	Tomb-dependent rec	324	96.5	2.8	2823	2	F87908	probable T223.8 (i
252	98.5	2.8	1043	2	T19734	hypothetical prote	325	96.5	2.8	2823	2	T23064	hypothetical prote
253	98.5	2.8	1232	2	S40766	hypothetical prote	326	96.5	2.8	3102	2	T43291	laminin alpha chain
254	98.5	2.8	2298	2	T49648	hypothetical prote	327	96.5	2.8	3144	2	A46068	Huntington disease
255	98	2.8	294	2	A37232	mucin, tracheal (A	328	96	2.7	273	2	A84332	hypothetical prote
256	98	2.8	376	2	T20972	hypothetical prote	329	96	2.7	327	2	E70180	hypothetical prote
257	98	2.8	438	2	B69023	conserved hypotnet	330	96	2.7	450	2	T17234	hypothetical prote
258	98	2.8	460	2	T45968	hypothetical prote	331	96	2.7	510	2	H84824	hypothetical prote
259	98	2.8	543	2	S56830	probable purine nu	332	96	2.7	559	2	S60473	En/Spm-like transp
260	98	2.8	559	2	S04531	thrombospondin-rel	333	96	2.7	583	2	T12574	phosphoglycerate m
261	98	2.8	581	2	S63183	CNN1 protein - yea	334	96	2.7	613	2	T36922	probable large sec
262	98	2.8	655	2	E81948	probable ATP-depen	335	96	2.7	705	2	T31261	hypothetical prote
263	98	2.8	726	2	T40790	probable permease	336	96	2.7	716	2	T32698	hypothetical prote
264	98	2.8	1020	2	T29108	hypothetical prote	337	96	2.7	740	1	B65136	YnfG protein - Esc
265	98	2.8	1088	1	IUX1NL	neural cell adhesi	338	96	2.7	740	2	H86005	hypothetical prote
266	98	2.8	1106	1	CHRA2	calcium channel pr	339	96	2.7	740	2	A98160	hypothetical prote
267	98	2.8	1291	2	S44983	vacuolating cyto	340	96	2.7	781	2	T41551	hypothetical prote
268	98	2.8	2440	2	S39162	transcriptional coc	341	96	2.7	867	2	JH0225	I66 protein - Tipu
269	97.5	2.8	340	2	B83262	hypothetical prote	342	96	2.7	873	2	F96615	probable Myb-famil
270	97.5	2.8	359	2	S42787	serine/threonine-r	343	96	2.7	896	2	S36326	ciathrin assembly
271	97.5	2.8	412	2	T35514	probable glycosyl	344	96	2.7	910	2	S68983	auxilin - bovine
272	97.5	2.8	499	2	S09880	hypothetical prote	345	96	2.7	946	2	JC5575	inter-alpha-lypsi
273	97.5	2.8	568	2	UC7317	cyclin-dependent x	346	96	2.7	1076	2	A35622	nuclear pore prote
274	97.5	2.8	670	2	T00083	hypothetical prote	347	96	2.7	1125	2	B41206	microtubule-associ
275	97.5	2.8	686	2	A38235	microtubule-associ	348	96	2.7	1392	2	A43336	microtubule-vesicl
276	97.5	2.8	823	2	A36378	probable transcrip	349	96	2.7	1456	2	S14005	hypothetical prote
277	97.5	2.8	882	2	B96931	hypothetical prote	350	96	2.7	3421	1	WZB566	367K tegument prot
278	97.5	2.8	882	2	AC2082	ferric aerobactin	351	95.5	2.7	316	2	T34553	hypothetical prote
279	97.5	2.8	916	2	F97053	penicillin-binding	352	95.5	2.7	391	2	E84392	aspartate aminotra
280	97.5	2.8	926	2	T48391	protein kinase-Iik	353	95.5	2.7	462	1	QOBE94	HHRF4 protein - hu
281	97.5	2.8	1129	2	S52631	phytochrome A - pa	354	95.5	2.7	521	2	C96700	nuclear pore compl
282	97.5	2.8	1288	2	E71884	vacuolating cyto	355	95.5	2.7	526	2	A56573	long-chain-fatty-a
283	97.5	2.8	1711	2	AB1283	extracellular link	356	95.5	2.7	566	2	H82132	hypothetical prote
284	97.5	2.8	1879	2	S74915	naescent polypeptid	357	95.5	2.7	635	2	F75477	Viral replicase 1
285	97.5	2.8	2187	2	T10826	kinase-related pro	358	95.5	2.7	653	2	JQ1241	cellulase (EC 3.2.
286	97.5	2.8	2311	1	TVCHSR	hypothetical prote	359	95.5	2.7	1039	1	S02711	transcription-repa
287	97.5	2.8	2957	2	T33152	42K membrane glyco	360	95.5	2.7	1177	1	S66085	vacuolating cyto
288	97	2.8	407	2	I52703	microtubule-associ	361	95.5	2.7	1287	2	B53739	semaphorin recepto
289	97	2.8	472	2	I67793	cell cycle regulat	362	95.5	2.7	1568	2	T09074	probable polyketid
290	97	2.8	623	2	A48123	pectate lyase (EC	363	95.5	2.7	1762	2	T03222	hypothetical diver
291	97	2.8	677	2	UC7303	endopeptidase Clp	364	95.5	2.7	1794	1	T38459	pyrimidine synthe
292	97	2.8	758	1	SUECCA	ATP-binding compon	365	95	2.7	2225	2	A23443	hypothetical prote
293	97	2.8	758	2	H90749	cell division prot	366	95	2.7	417	2	A12003	hypothetical prote
294	97	2.8	758	2	D85600	autotransporter pr	367	95	2.7	472	2	T24618	homoserine O-acety
295	97	2.8	806	2	F72024	cell division prote	368	95	2.7	518	1	XY1MHA	probable aminopept
296	97	2.8	806	2	F86600	conserved hypotnet	369	95	2.7	536	2	B83278	hypothetical prote
297	97	2.8	868	2	AF3204	phosphoprotein, sy	370	95	2.7	544	2	H72647	probable dual spec
298	97	2.8	870	2	F69406	cardamomyl-phosphat	371	95	2.7	597	1	S43743	zinc-finger trans
299	97	2.8	881	2	F69438	subunit A of ATP-d	372	95	2.7	641	2	JC6017	outer membrane pro
300	97	2.8	896	2	T22061	exopolysaccharona	373	95	2.7	676	1	S69783	hypothetical prote
301	97	2.8	901	2	A44825	tuberos sclerosiis	374	95	2.7	742	2	AH2166	conserved hypotnet
302	97	2.8	901	2	AD3317	hypothetical prote	375	95	2.7	747	2	T39744	calcium-binding pr
303	97	2.8	1162	2	DB6625	beta-xylosidase-li	376	95	2.7	824	2	T36818	glycoprotein 350/2
304	97	2.8	1203	2	F83711	probable membrane	377	95	2.7	824	2	A47282	penicillin-binding
305	97	2.8	1376	2	F83711	complement factor	378	95	2.7	872	2	T33717	fibronectin-bindin
306	97	2.8	1784	2	A49420	PO9G.8 protein -	379	95	2.7	1092	2	T33717	endo-1,4-beta-xyla
307	96.5	2.8	409	2	T18726	hypothetical prote	380	95	2.7	1184	2	S36868	cardamomyl-phosphat
308	96.5	2.8	533	1	JU0146	hypothetical prote	381	95	2.7	1184	2	S50832	alpha, alpha-trehal
309	96.5	2.8	542	2	S64030	serine proteinase	382	95	2.7	125	2	G97053	atrophin-1 - human
310	96.5	2.8	670	2	S67383	probable membrane	383	95	2.7	1025	2	S69790	atrophin-1 - human
311	96.5	2.8	746	1	S44792	probable signal tr	384	95	2.7	1063	2	T00624	major merozoite su
312	96.5	2.8	764	1	BBHU	PO9G.8 protein -	385	95	2.7	1092	2	T33717	apoptotein(a) (EC
313	96.5	2.8	773	2	T49925	beta-xylosidase-li	386	95	2.7	1184	2	G01763	mucin, submaxillar
314	96.5	2.8	803	2	T18738	hypothetical prote	387	95	2.7	1184	2	A45546	bcsA 5'-region pro
315	96.5	2.8	829	2	D71485	probable adenylate	388	95	2.7	13288	2	T03099	capsid-associated
316	96.5	2.8	867	2	B84417	cell surface glyco	389	95	2.7	4548	1	S00657	conserved hypotnet
317	96.5	2.8	867	2	AD1856	hypothetical prote	390	94.5	2.7	4548	1	S00657	hypothetical serin
318	96.5	2.8	918	2	T02759	hypothetical prote	391	94.5	2.7	474	2	B36963	beta1-syntrophin -
319	96.5	2.8	1013	2	B75583	hypothetical prote	392	94.5	2.7	502	2	G87433	
320	96.5	2.8	1032	2	T13433	transcription fact	393	94.5	2.7	530	2	S62439	
321	96.5	2.8	1037	2	T13350	high molecular mas	394	94.5	2.7	538	2	I59291	

395	94.5	2.7	699	2	C43674	US4 protein - huma	468	93	2.7	1526	2	S49763	gingipain R (EC 3.
396	94.5	2.7	704	2	A30411	synapsin Ia - rat	469	93	2.7	1611	2	T38236	hypothetical prote
397	94.5	2.7	705	2	H89900	translacton initia	470	93	2.7	1792	2	A57075	tensin - chicken (
398	94.5	2.7	734	2	S44617	CS0C3.11 protein -	471	93	2.7	1820	2	A55494	latent transformin
399	94.5	2.7	856	2	T43631	serine/threonine k	472	93	2.7	2468	2	A83412	hypothetical prote
400	94.5	2.7	875	2	T12794	hypothetical yomg	473	93	2.7	3433	1	GNMYKV	genome polyprotein
401	94.5	2.7	876	1	A57988	regulatory protein	474	93	2.7	4688	2	F82885	hypothetical prote
402	94.5	2.7	913	2	S20590	exo-alpha-sialidas	475	92.5	2.6	487	2	D64551	outer membrane pro
403	94.5	2.7	924	2	A44945	104K microne-m-rho	476	92.5	2.6	508	2	A32225	nerve growth facto
404	94.5	2.7	1185	2	T19212	hypothetical prote	477	92.5	2.6	563	2	J00623	nerve growth facto
405	94.5	2.7	1282	2	JC4393	microbial collagen	478	92.5	2.6	581	2	E91165	gamma-glutamyltran
406	94.5	2.7	1306	2	S25370	M8B2 protein - yea	479	92.5	2.6	581	2	E86011	gamma-glutamyltran
407	94.5	2.7	1487	1	EDBE81	immediate-early pr	480	92.5	2.6	639	2	E98281	cobr protein (impo
408	94.5	2.7	3104	2	S20473	fatty-acid synthas	481	92.5	2.6	639	2	AC3002	cobryntic acid syn
409	94.5	2.7	3890	2	C89921	hypothetical prote	482	92.5	2.6	662	2	T51948	omnipotent nonsens
410	94	2.7	403	2	C70832	hypothetical prote	483	92.5	2.6	756	2	G64150	P22M8.3 protein -
411	94	2.7	483	2	F83205	probable lyase PA3	484	92.5	2.6	772	2	S62481	hypothetical prote
412	94	2.7	509	1	O4RT0	laurate omega-hydr	485	92.5	2.6	779	2	A57177	NIMA-like protein
413	94	2.7	642	2	T39607	fork head protein	486	92.5	2.6	784	2	S26538	SPR-1 protein - hu
414	94	2.7	649	1	B37953	transcription regu	487	92.5	2.6	860	2	JC4566	chitinase (EC 3.2.
415	94	2.7	678	2	G65104	hypothetical 72.8	488	92.5	2.6	946	2	S27921	nuclear antigen Eb
416	94	2.7	754	2	T14877	hypothetical prote	489	92.5	2.6	1023	2	JC4013	major acidic nucle
417	94	2.7	774	2	D97527	ompl protein precu	490	92.5	2.6	1238	2	T40120	C2H2 type zinc fin
418	94	2.7	774	2	D97527	group 1 outer memb	491	92.5	2.6	1325	2	S16429	dynein-associated
419	94	2.7	903	2	A62746	hypothetical prote	492	92.5	2.6	1844	2	S01956	hypothetical prote
420	94	2.7	928	2	E84483	hypothetical prote	493	92.5	2.6	1985	2	S19151	hypothetical prote
421	94	2.7	948	2	T11678	hypothetical prote	494	92.5	2.6	2357	2	A59249	class VII unconven
422	94	2.7	951	2	T26738	hypothetical prote	495	92.5	2.6	2588	2	T14342	NSD1 protein - mou
423	94	2.7	975	2	T26737	hypothetical prote	496	92.5	2.6	3083	2	AH2493	hypothetical prote
424	94	2.7	1080	2	S48944	hypothetical prote	497	92.5	2.6	3924	2	S37431	ankyrin 2, neuron
425	94	2.7	1163	2	D82202	vggr protein VC41	498	92	2.6	270	2	AH2435	hypothetical prote
426	94	2.7	1225	2	T48251	ubiquitin-protein	499	92	2.6	427	2	A53798	58K membrane-assoc
427	94	2.7	1262	1	B48758	protein-tyrosine-p	500	92	2.6	509	2	S47553	cytochrome P450 Cy
428	94	2.7	1496	1	A48758	pyroline-lysine-p	501	92	2.6	540	1	FOWVHL	gag polyprotein -
429	94	2.7	1520	2	AF3008	polyketide synthas	502	92	2.6	550	2	G70597	probable proteinas
430	94	2.7	1520	2	G98275	hypothetical prote	503	92	2.6	561	2	T14792	hypothetical prote
431	94	2.7	1547	2	T28657	blackjack protein,	504	92	2.6	567	2	S76847	phosphoglucomutase
432	94	2.7	1578	2	AD1512	peptidoglycan bou	505	92	2.6	591	1	S30145	ketol-acid reducto
433	93.5	2.7	580	1	EKECEX	gamma-glutamyltran	506	92	2.6	591	1	T45681	ketol-acid reducto
434	93.5	2.7	638	2	A29440	signal recognition	507	92	2.6	681	2	A45705	type I transmembra
435	93.5	2.7	666	2	B70803	hypothetical prote	508	92	2.6	712	2	G02512	interleukin-1 rece
436	93.5	2.7	681	1	F85062	hypothetical prote	509	92	2.6	747	2	T23507	hypothetical prote
437	93.5	2.7	839	1	GNM52	genome polyprotein	510	92	2.6	784	2	AF1638	DNA translocase ho
438	93.5	2.7	841	2	E71808	probable iron (III	511	92	2.6	880	2	AF2128	hypothetical prote
439	93.5	2.7	918	2	C84720	hypothetical prote	512	92	2.6	907	1	QOBR21	membrane antigen g
440	93.5	2.7	924	2	H85354	hypothetical prote	513	92	2.6	937	2	T40723	c-1-tetrahydrofola
441	93.5	2.7	981	1	FOMVGM	gag-abl polyprotei	514	92	2.6	946	2	SS4354	inter-alpha-inhibi
442	93.5	2.7	1116	2	B88612	protein Y76A2A.2 (	515	92	2.6	1046	2	S67786	hypothetical prote
443	93.5	2.7	1238	1	JC5573	copper-transporin	516	92	2.6	1092	2	T18305	replication factor
444	93.5	2.7	1487	1	EDBER6	155K transcription	517	92	2.6	1092	2	T18306	replication factor
445	93.5	2.7	1616	2	T17884	S-layer protein -	518	92	2.6	1123	2	S20497	phytochrome A - po
446	93.5	2.7	2274	2	T30258	adenomatus polypo	519	92	2.6	1124	1	FKPUZ	phytochrome - zucc
447	93.5	2.7	2731	1	VFIHJH	genome polyprotein	520	92	2.6	1135	2	T30561	Scythe protein - A
448	93.5	2.7	4735	2	T17463	rifamycin polyketi	521	92	2.6	1208	2	S17286	period clock prote
449	93	2.7	260	2	C83362	hypothetical prote	522	92	2.6	1224	2	T14007	microtubule-associ
450	93	2.7	302	2	D85253	hypothetical prote	523	92	2.6	1231	2	T30841	serine-repeat anti
451	93	2.7	432	2	J50306	microtubule-associ	524	92	2.6	1237	2	A54080	protein-tyrosine-p
452	93	2.7	504	2	AG2373	hypothetical prote	525	92	2.6	1336	2	S36851	L-shaped tail fibe
453	93	2.7	533	2	J50304	developmental cont	526	92	2.6	1788	2	AH1447	probable tape-meas
454	93	2.7	574	2	A46283	sporozolite surface	527	92	2.6	2136	2	B84651	hypothetical prote
455	93	2.7	627	1	JC6534	protein kinase 1 (	528	92	2.6	2254	2	D86215	hypothetical prote
456	93	2.7	675	2	E83075	probable cytochrom	529	92	2.6	2843	1	R8H0AP	adenomatus polypo
457	93	2.7	767	2	A82882	cell division prot	530	92	2.6	3449	2	T01083	hypothetical prote
458	93	2.7	775	2	I49759	hepatocyte growth	531	92	2.6	3507	2	T34513	hypothetical prote
459	93	2.7	836	2	S49940	cell division cont	532	92	2.6	249	2	T21083	hypothetical prote
460	93	2.7	917	2	B85057	hypothetical prote	533	91.5	2.6	259	2	H75349	hypothetical prote
461	93	2.7	953	2	T12577	H+-exporting ATPas	534	91.5	2.6	278	2	S53363	uv excision repair
462	93	2.7	973	2	T18341	icmf protein - Leg	535	91.5	2.6	368	2	T40115	conserved hypotet
463	93	2.7	1159	1	A44280	inner layer protei	536	91.5	2.6	374	2	C97965	probable phosphoma
464	93	2.7	1234	2	C97606	hypothetical prote	537	91.5	2.6	468	2	D87004	probable transcrip
465	93	2.7	1234	2	AE2828	conserved hypotet	538	91.5	2.6	474	2	E83392	probable outer mem
466	93	2.7	1278	2	T27925	hypothetical prote	539	91.5	2.6	479	2	G71957	chitinase (EC 3.2.
467	93	2.7	1390	2	T31353	polypeptide - Arab	540	91.5	2.6	542	2	I39540	

541	91.5	2.6	562	2	S38145	614	90.5	2.6	466	2	AF0224	flagellar hook-ass
542	91.5	2.6	627	2	S68958	615	90.5	2.6	472	2	T48074	hypothetical prote
543	91.5	2.6	639	2	S20139	616	90.5	2.6	526	2	C84223	methionyl-CoA
544	91.5	2.6	653	2	E84682	617	90.5	2.6	565	1	HMIIVD8	hemagglutinin prec
545	91.5	2.6	674	2	A97490	618	90.5	2.6	571	2	T43456	hypothetical prote
546	91.5	2.6	703	2	T41065	619	90.5	2.6	580	2	AB0994	gamma-glutamyltran
547	91.5	2.6	793	2	S59067	620	90.5	2.6	600	2	E53290	oligopeptide trans
548	91.5	2.6	852	2	A28459	621	90.5	2.6	642	1	HHBVA1	dhak-type molecula
549	91.5	2.6	863	2	A12077	622	90.5	2.6	645	2	S41372	hypothetical RNA-b
550	91.5	2.6	943	2	T16768	623	90.5	2.6	654	2	T41584	hypothetical prote
551	91.5	2.6	957	2	S32903	624	90.5	2.6	671	2	AC1407	transketolase homo
552	91.5	2.6	1052	2	T14343	625	90.5	2.6	782	2	S27833	iron(III) dicitrat
553	91.5	2.6	1079	2	T10996	626	90.5	2.6	842	2	H64694	FeMB-dependent rec
554	91.5	2.6	1104	2	UN0635	627	90.5	2.6	847	2	C87678	membrane glycoprot
555	91.5	2.6	1290	2	S59310	628	90.5	2.6	867	2	T45463	SH3 domains-contai
556	91.5	2.6	1323	2	G64630	629	90.5	2.6	892	2	T09071	hypothetical prote
557	91.5	2.6	1355	2	T30253	630	90.5	2.6	934	2	E64235	hypothetical prote
558	91.5	2.6	1355	2	T00075	631	90.5	2.6	936	2	T23393	hypothetical prote
559	91.5	2.6	1433	2	T30261	632	90.5	2.6	1029	2	H86179	hypothetical prote
560	91.5	2.6	1751	2	A45604	633	90.5	2.6	1091	2	S63046	hypothetical prote
561	91.5	2.6	1993	2	AF1450	634	90.5	2.6	1075	2	A57377	transcription fact
562	91.5	2.6	2109	1	I50421	635	90.5	2.6	1075	2	AS7370	ceramoyl-phosphat
563	91.5	2.6	2124	2	A28452	636	90.5	2.6	1083	2	S59780	hypothetical prote
564	91.5	2.6	3263	2	B82410	637	90.5	2.6	1183	2	S63046	probable membrane
565	91.5	2.6	3562	2	A47171	638	90.5	2.6	1234	2	T30160	hypothetical prote
566	91	2.6	168	2	G89026	639	90.5	2.6	1250	2	T27706	hypothetical prote
567	91	2.6	338	2	B64336	640	90.5	2.6	1357	2	T29265	hypothetical prote
568	91	2.6	350	2	AD0466	641	90.5	2.6	1609	1	MMHUB2	laminin gamma-1 ch
569	91	2.6	374	2	S46254	642	90.5	2.6	1946	2	AE1449	hypothetical prote
570	91	2.6	452	2	S75956	643	90.5	2.6	2044	2	AB1180	probable peptidogl
571	91	2.6	488	2	T09138	644	90.5	2.6	2126	2	E70522	probable polyketid
572	91	2.6	503	2	T39375	645	90.5	2.6	3869	2	A48205	All-1 protein +GRE
573	91	2.6	524	2	AG1455	646	90.5	2.6	340	2	E70121	hypothetical prote
574	91	2.6	524	2	AH1091	647	90	2.6	348	2	J00431	hypothetical 35.5K
575	91	2.6	530	2	T32812	648	90	2.6	356	2	D82643	conserved hypotnet
576	91	2.6	539	2	G72593	649	90	2.6	364	2	A28820	microtubule-associ
577	91	2.6	559	2	B56791	650	90	2.6	397	2	S46691	exopolysphatase
578	91	2.6	583	2	S67571	651	90	2.6	414	2	T09589	probable cdc2-like
579	91	2.6	600	2	T39516	652	90	2.6	428	2	S61623	hypothetical prote
580	91	2.6	627	2	AE1818	653	90	2.6	473	2	S50755	hypothetical prote
581	91	2.6	650	2	T04487	654	90	2.6	491	2	F95010	ABC transporter, b
582	91	2.6	655	1	A55726	655	90	2.6	498	2	S45567	nuclear factor I-A
583	91	2.6	678	2	D91132	656	90	2.6	509	2	S45565	nuclear factor I-A
584	91	2.6	678	2	G85977	657	90	2.6	514	2	C97882	hypothetical prote
585	91	2.6	783	2	E97340	658	90	2.6	561	2	C84721	hypothetical prote
586	91	2.6	791	2	AC0017	659	90	2.6	566	1	HMIIVT8	hemagglutinin prec
587	91	2.6	847	2	F96531	660	90	2.6	580	2	F84471	hypothetical prote
588	91	2.6	866	2	G86946	661	90	2.6	593	2	A96783	unknown protein F2
589	91	2.6	896	2	S50752	662	90	2.6	600	2	T06292	hypothetical prote
590	91	2.6	952	2	F86160	663	90	2.6	610	2	PN0012	mucin 4, tracheal
591	91	2.6	983	2	A12284	664	90	2.6	658	2	A86231	hypothetical prote
592	91	2.6	1039	2	A33183	665	90	2.6	675	2	D65083	myrein-lipoprotein
593	91	2.6	1152	2	B83566	666	90	2.6	677	2	US0178	protein kinase YKR
594	91	2.6	1226	1	S65593	667	90	2.6	799	2	C82929	ATP synthase alpha
595	91	2.6	1260	2	S60896	668	90	2.6	838	2	T08423	Axin homolog Axil1
596	91	2.6	1268	2	S33411	669	90	2.6	905	2	T38314	probable vacuolar
597	91	2.6	1275	2	T33369	670	90	2.6	949	1	PXMUP1	H+-exporting ATPas
598	91	2.6	1307	2	T30887	671	90	2.6	1018	2	T40253	hypothetical prote
599	91	2.6	1456	1	MMKGPV	672	90	2.6	1049	2	C95883	probable efflux pr
600	91	2.6	1473	2	A35186	673	90	2.6	1088	2	T08599	probable transcrip
601	91	2.6	1553	2	T03301	674	90	2.6	1164	2	T03814	tumor suppressor p
602	91	2.6	1662	2	T18540	675	90	2.6	1426	2	E90456	oxydoreductase, pr
603	91	2.6	1662	2	H96597	676	90	2.6	1522	2	T39371	transcription regu
604	91	2.6	2090	2	S26058	677	90	2.6	1545	2	S48824	probable membrane
605	91	2.6	2466	2	I67629	678	90	2.6	1589	2	T42233	submaxillary mucin
606	91	2.6	2688	2	I49477	679	90	2.6	1692	2	G01449	probable mucin G2
607	91	2.6	3436	2	D71917	680	90	2.6	1832	2	T31113	mucin-like glycopr
608	91	2.6	3436	2	S55659	681	90	2.6	1894	2	D86452	protein F6N18.13 [
609	91	2.6	243	2	AD2470	682	90	2.6	2500	1	MMHUB2	HIV-BP2 enhancer-b
610	90.5	2.6	316	2	B41710	683	90	2.6	2559	2	T09144	probable guanine n
611	90.5	2.6	351	2	G84128	684	90	2.6	3034	2	T14119	seven-pass transme
612	90.5	2.6	399	2	T18853	685	90	2.6	4006	2	T09070	probable tenascin
613	90.5	2.6	435	2	G69404	686	90	2.6	5291	2	F90696	hypothetical prote

687	89.5	2.6	336	2	AH0201	probable zinc-bind	760	89	2.5	1159	2	S62562	probable nuclear p
688	89.5	2.6	364	2	T24153	hypothetical prote	761	89	2.5	1164	2	S46769	hypothetical prote
689	89.5	2.6	397	2	T40539	zinc finger protei	762	89	2.5	1194	2	E96624	hypothetical prote
690	89.5	2.6	409	2	A70932	probable PPE prote	763	89	2.5	1224	2	T40765	webl protein homol
691	89.5	2.6	420	2	S76691	hypothetical prote	764	89	2.5	1234	2	T31623	hypothetical prote
692	89.5	2.6	428	2	G81352	3-phosphoshikimate	765	89	2.5	1257	2	S28764	neurocan precursor
693	89.5	2.6	435	2	C70456	homoserine dehydro	766	89	2.5	1372	2	T29309	hypothetical prote
694	89.5	2.6	482	2	T36045	hypothetical prote	767	89	2.5	1445	2	A59437	hypothetical prote
695	89.5	2.6	522	2	S41819	nucliosporin p62 -	768	89	2.5	1643	2	T07961	myosin heavy chain
696	89.5	2.6	532	2	S74453	hypothetical prote	769	89	2.5	1737	2	A59235	unconventional myo
697	89.5	2.6	539	2	D82765	N-acetyluramoyl-L	770	89	2.5	1823	2	S28974	vitellogenin precu
698	89.5	2.6	566	2	T29695	hypothetical prote	771	89	2.5	1859	1	A34092	DNA-directed RNA p
699	89.5	2.6	594	1	D55514	dihydroilipoamide d	772	89	2.5	1862	2	T29959	DNA-directed RNA p
700	89.5	2.6	594	2	C71661	penicillin-binding d	773	89	2.5	2344	1	RRWRH	genome polyprotein
701	89.5	2.6	636	2	I48718	poly(A)-binding pr	774	89	2.5	2344	2	S55399	genome polyprotein
702	89.5	2.6	648	1	P3BP6	p3 protein - phage	775	89	2.5	2649	2	T51023	hypothetical prote
703	89.5	2.6	660	2	T03038	probable inhibitor	776	89	2.5	3030	2	A43932	muscin 2 precursor
704	89.5	2.6	712	2	B87683	TonB-dependent rec	777	89	2.5	3624	2	AD0835	large repetitive p
705	89.5	2.6	728	2	T38220	hypothetical prote	778	89	2.5	4543	1	A53102	alpha-2-macroglobu
706	89.5	2.6	760	2	A82225	hypothetical prote	779	89	2.5	4957	2	T03455	ALR protein - huma
707	89.5	2.6	761	2	T41304	probable rna-bindi	780	89	2.5	5188	2	B85547	probable RTX fam1
708	89.5	2.6	766	2	T11650	sak1 protein - fis	781	89	2.5	5262	2	T03454	ALR protein - huma
709	89.5	2.6	779	1	S40382	box A-binding fact	782	88.5	2.5	399	2	G83891	spore germination
710	89.5	2.6	790	2	T34293	hypothetical prote	783	88.5	2.5	443	2	T48708	hypothetical prote
711	89.5	2.6	837	2	T00355	hypothetical prote	784	88.5	2.5	457	2	H85013	hypothetical prote
712	89.5	2.6	866	2	S74291	cytokine receptor	785	88.5	2.5	473	2	E72715	probable aspartate
713	89.5	2.6	896	1	A35782	hypothetical prote	786	88.5	2.5	476	2	G90512	p60-like (mycoplas
714	89.5	2.6	901	2	A49227	sialidase - Actino	787	88.5	2.5	532	2	B35621	spore germination
715	89.5	2.6	924	2	T25007	hypothetical prote	788	88.5	2.5	532	2	AE1964	snare-type molecula
716	89.5	2.6	927	2	T24031	hypothetical prote	789	88.5	2.5	558	2	G96522	glucocorticoid rec
717	89.5	2.6	975	1	A28174	methylesterhydr	790	88.5	2.5	674	2	B71438	FKBP17.16 (impor
718	89.5	2.6	982	2	A53253	microtubule-associ	791	88.5	2.5	721	2	D82934	ATP-dependent zinc
719	89.5	2.6	993	2	C90072	hypothetical prote	792	88.5	2.5	748	2	T04011	hypothetical prote
720	89.5	2.6	1008	2	T41244	SEC14 protein homo	793	88.5	2.5	771	2	A54273	glucocorticoid rec
721	89.5	2.6	1050	2	S25363	translation elonga	794	88.5	2.5	797	1	VEBEX1	glycoprotein x pre
722	89.5	2.6	1051	2	T51904	hypothetical prote	795	88.5	2.5	800	2	AE3151	glucosylase (lipo
723	89.5	2.6	1058	2	A38564	ubiquitin-protein	796	88.5	2.5	819	2	A53714	proteas kinase (EC
724	89.5	2.6	1208	2	T09049	competence factor	797	88.5	2.5	837	2	AB3383	hypothetical membr
725	89.5	2.6	1261	2	S75130	sensory transducti	798	88.5	2.5	861	2	S77409	hypothetical prote
726	89.5	2.6	1298	1	EDBE75	immediate-early pr	799	88.5	2.5	885	1	S26723	DNA-directed RNA p
727	89.5	2.6	1460	2	T00095	hypothetical prote	800	88.5	2.5	954	2	T19765	hypothetical prote
728	89.5	2.6	1463	2	T30193	nuclear receptor c	801	88.5	2.5	976	2	G87389	TonB-dependent rec
729	89.5	2.6	1530	2	AD1663	glutamate synthase	802	88.5	2.5	1014	2	A55260	cytotoxic necrotiz
730	89.5	2.6	1544	2	T04464	hypothetical prote	803	88.5	2.5	1021	2	T05108	hypothetical prote
731	89.5	2.6	1734	2	A54602	microtubule-associ	804	88.5	2.5	1073	1	T08298	plasmid replicatio
732	89.5	2.6	2475	2	S35307	polyprotein pp220	805	88.5	2.5	1166	2	T29099	reverse gyrase - S
733	89.5	2.6	2606	2	T03159	large tegument pro	806	88.5	2.5	1274	2	S55050	cardiac myosin-bin
734	89.5	2.6	3283	2	AC1018	large repetitive p	807	88.5	2.5	1293	2	T30871	orsellinic acid sy
735	89.5	2.6	7463	2	T36248	CNA peptide synthe	808	88.5	2.5	1475	2	S42718	nuclear pore compl
736	89	2.5	261	2	A83829	thiamin biosynthes	809	88.5	2.5	1778	2	AF1116	internalin protein
737	89	2.5	336	2	F95044	FMN-dependent dehy	810	88.5	2.5	1844	1	RRWPTM	genome polyprotein
738	89	2.5	336	2	E97914	isopectenyl diphos	811	88.5	2.5	2251	2	T24490	hypothetical prote
739	89	2.5	376	2	G70301	N-acetylornithine	812	88.5	2.5	2761	2	T21064	hypothetical prote
740	89	2.5	524	2	D82944	hypothetical membr	813	88.5	2.5	2783	1	A41948	alpha-fetoprotein
741	89	2.5	539	2	H72422	hypothetical prote	814	88.5	2.5	3282	2	E82750	hemagglutinin-like
742	89	2.5	546	2	G64803	phosphoglucumutase	815	88.5	2.5	3442	2	E82589	hemagglutinin-like
743	89	2.5	559	2	A42807	phosphoglycerate m	816	88.5	2.5	3455	2	B82519	hemagglutinin-like
744	89	2.5	560	2	D30930	flagellar basal bo	817	88.5	2.5	4385	2	T29042	hypothetical prote
745	89	2.5	593	2	T38547	probable cell divi	818	88.5	2.5	5147	1	IJFPTM	cadherin-related t
746	89	2.5	609	1	A48070	heat shock transcr	819	88.5	2.5	5825	2	T12117	polyprotein - fava
747	89	2.5	651	2	E86242	hypothetical prote	820	88	2.5	329	2	S31580	storage protein, b
748	89	2.5	688	2	T18263	S-layer protein -	821	88	2.5	341	2	B28820	microtubule-associ
749	89	2.5	733	2	A45301	microtubule-associ	822	88	2.5	369	2	G83434	translocation prot
750	89	2.5	770	2	T22808	hypothetical prote	823	88	2.5	381	2	T52434	hypothetical prote
751	89	2.5	862	2	S53913	FKB2 protein - Yea	824	88	2.5	459	2	JC7931	cellobiohydrolase
752	89	2.5	865	1	S02196	DNA-directed RNA p	825	88	2.5	465	2	G90961	flagellar capping
753	89	2.5	878	2	T21621	hypothetical prote	826	88	2.5	465	2	G85809	flagellar capping
754	89	2.5	927	2	F82818	conserved hypochet	827	88	2.5	468	2	A64956	flagellar hook-ass
755	89	2.5	929	2	T35683	ftsK homolog - Str	828	88	2.5	466	2	T49017	hypothetical prote
756	89	2.5	976	2	A87576	peptidase, M16 fam	829	88	2.5	521	2	S54266	glycoprotein GC -
757	89	2.5	1106	2	A97647	cation efflux syst	830	88	2.5	525	2	A35596	nuclear pore glyco
758	89	2.5	1106	2	AG2870	Acg family transpo	831	88	2.5	543	2	T33898	hypothetical prote
759	89	2.5	1145	2	B75625	hypothetical prote	832	88	2.5	562	2	A82743	probable malate de



979	86.5	2.5	547	2	T41213	1052	86	2.5	798	2	T34248	hypothetical prote
980	86.5	2.5	578	2	F86484	1053	86	2.5	802	1	B44390	protein-tyrosine-P
981	86.5	2.5	594	2	S62141	1054	86	2.5	810	2	C72785	probable aldehyde
982	86.5	2.5	648	2	T09036	1055	86	2.5	842	2	H86220	hypothetical prote
983	86.5	2.5	658	2	T39500	1056	86	2.5	926	2	T39664	chitin synthase 2
984	86.5	2.5	667	2	S74254	1057	86	2.5	932	2	T45894	hypothetical prote
985	86.5	2.5	685	2	T18964	1058	86	2.5	937	2	G87640	TonB-dependent rec
986	86.5	2.5	687	2	T09051	1059	86	2.5	954	2	H86174	protein F19P19.26
987	86.5	2.5	701	2	JC7164	1060	86	2.5	1027	2	F87370	alpha-L-rhamnosida
988	86.5	2.5	713	2	T44447	1061	86	2.5	1161	2	D83076	type 4 fimbrial bi
989	86.5	2.5	714	2	A83016	1062	86	2.5	1218	2	A26427	period clock prote
990	86.5	2.5	723	2	T38780	1063	86	2.5	1331	2	T04538	hypothetical prote
991	86.5	2.5	730	2	A96988	1064	86	2.5	1340	2	A39608	proteoglycan core
992	86.5	2.5	780	2	A48143	1065	86	2.5	1348	2	AH1115	cell surface prote
993	86.5	2.5	784	2	T20074	1066	86	2.5	1495	2	A85240	hypothetical prote
994	86.5	2.5	850	1	PNECA	1067	86	2.5	1495	2	T10649	hypothetical prote
995	86.5	2.5	850	2	T01847	1068	86	2.5	1702	2	T14050	protein kinase (EC
996	86.5	2.5	870	2	A89201	1069	86	2.5	1829	2	T14280	RN1 protein - mous
997	86.5	2.5	881	2	B98320	1070	86	2.5	1962	2	A32634	lactocepin (EC 3.4
998	86.5	2.5	886	1	GNLJSP	1071	86	2.5	2094	2	S33124	lpr protein - huma
999	86.5	2.5	908	1	S61476	1072	86	2.5	2256	2	AD1018	large repetitive P
1000	86.5	2.5	927	2	T38127	1073	86	2.5	2327	2	T42630	aggreacan - bovine
1001	86.5	2.5	1038	2	H90053	1074	86	2.5	2761	2	T29285	hypothetical prote
1002	86.5	2.5	1093	2	B86748	1075	86	2.5	3157	2	B70969	probable PPB prote
1003	86.5	2.5	1134	2	S53955	1076	86	2.5	3457	2	T42730	Bassoon protein -
1004	86.5	2.5	1180	2	E86719	1077	86	2.5	5105	2	T32650	hypothetical prote
1005	86.5	2.5	1249	2	T14150	1078	86	2.5	6260	2	T30228	polyketide synthas
1006	86.5	2.5	1269	2	A90267	1079	86	2.5	287	2	AB3395	biotin-lacetyl-CoA
1007	86.5	2.5	1344	2	T14316	1080	86	2.5	288	2	T21790	hypothetical prote
1008	86.5	2.5	1379	2	A81102	1081	86	2.5	319	2	B86433	hypothetical prote
1009	86.5	2.5	1462	1	A69809	1082	86	2.5	350	2	S61581	hypothetical prote
1010	86.5	2.5	1481	1	Q2DOP3	1083	86	2.5	364	2	T48188	gene NKX6.1 protel
1011	86.5	2.5	1513	2	A54895	1084	86	2.5	377	2	A48018	mucin 7 precursor,
1012	86.5	2.5	1537	2	S53465	1085	86	2.5	394	2	G84265	hypothetical prote
1013	86.5	2.5	1565	2	S04729	1086	86	2.5	430	2	S50604	AS12 protein - yea
1014	86.5	2.5	1733	2	S27939	1087	86	2.5	437	2	H64251	replicatoin initia
1015	86.5	2.5	1939	2	D97316	1088	86	2.5	451	2	A88641	protein F52C12.1
1016	86.5	2.5	2073	1	BWASBE	1089	86	2.5	467	2	E91043	ethanolamine utili
1017	86.5	2.5	2756	2	T30183	1090	86	2.5	467	2	H85887	ethanolamine utili
1018	86.5	2.5	4151	2	T13734	1091	86	2.5	522	2	S09996	nuclear factor I-A
1019	86	2.5	126	2	T21762	1092	86	2.5	548	2	T32907	hypothetical prote
1020	86	2.5	168	2	S52994	1093	86	2.5	561	2	A31256	transcription fac
1021	86	2.5	226	2	T29210	1094	86	2.5	567	2	A62008	hypothetical prote
1022	86	2.5	289	2	E81259	1095	86	2.5	576	2	A26628	homeotic protein I
1023	86	2.5	344	2	T48827	1096	86	2.5	601	2	T31466	cell-division proc
1024	86	2.5	350	1	C70009	1097	86	2.5	616	2	AF0263	proteinase IV (EC
1025	86	2.5	384	2	T32756	1098	86	2.5	624	2	T33868	hypothetical prote
1026	86	2.5	413	2	S28066	1099	86	2.5	659	2	C65022	yfgG protein - Ebc
1027	86	2.5	420	2	UC4716	1100	86	2.5	671	2	AC1183	transketolase homo
1028	86	2.5	424	2	T33663	1101	86	2.5	695	2	D90468	copper-transportin
1029	86	2.5	442	2	G85878	1102	86	2.5	698	2	T17261	hypothetical prote
1030	86	2.5	442	2	E91034	1103	86	2.5	718	2	G97249	transcription acce
1031	86	2.5	461	2	S45568	1104	86	2.5	730	2	T16455	hypothetical prote
1032	86	2.5	462	2	AH1184	1105	86	2.5	734	2	T52535	suppressor of A-ki
1033	86	2.5	494	2	H75387	1106	86	2.5	747	2	B85499	outer membrane rec
1034	86	2.5	508	2	E70764	1107	86	2.5	747	2	B90648	outer membrane rec
1035	86	2.5	509	2	UC5428	1108	86	2.5	758	2	A29253	finger protein hun
1036	86	2.5	532	2	B36596	1109	86	2.5	806	2	B69637	DNA gyrase-like pr
1037	86	2.5	538	2	S57459	1110	86	2.5	825	2	T29634	hypothetical prote
1038	86	2.5	563	2	C97348	1111	86	2.5	832	2	AD1096	internalin protein
1039	86	2.5	567	1	HMIIV	1112	86	2.5	866	1	UC5085	replication licens
1040	86	2.5	575	2	T28230	1113	86	2.5	904	2	AH2019	hypothetical prote
1041	86	2.5	601	1	ORMSN1	1114	86	2.5	922	2	F81539	polymorphic membra
1042	86	2.5	638	2	T38863	1115	86	2.5	922	2	B72131	polymorphic outer
1043	86	2.5	647	2	A84265	1116	86	2.5	922	2	E86491	polymorphic outer
1044	86	2.5	658	2	A33598	1117	86	2.5	927	2	AH1369	transmembrane prot
1045	86	2.5	672	2	T20310	1118	86	2.5	930	2	T08817	hypothetical prote
1046	86	2.5	702	2	S48754	1119	86	2.5	1001	2	T13807	potassium channel
1047	86	2.5	704	2	S25820	1120	86	2.5	1037	2	T050309	probable glycine d
1048	86	2.5	734	2	T42588	1121	86	2.5	1054	2	T43226	translacion initia
1049	86	2.5	738	2	T44194	1122	86	2.5	1131	2	T15787	hypothetical prote
1050	86	2.5	740	2	AD0485	1123	86	2.5	1133	2	T22976	hypothetical prote
1051	86	2.5	795	2	T36588	1124	86	2.5	1139	2	B54962	sterol regulatory



1125	85.5	2.4	1142	2	S36845	1198	85	2.4	1289	2	T18212	paraasporal crystal
1126	85.5	2.4	1147	2	T40866	1199	85	2.4	1334	2	T50568	probable multi-dom
1127	85.5	2.4	1182	2	S14916	1200	85	2.4	1495	2	S60255	transcription co-r
1128	85.5	2.4	1221	2	T23472	1201	85	2.4	1582	2	AC1153	adhesin homolog lm
1129	85.5	2.4	1241	2	T18311	1202	85	2.4	1633	2	T01879	hypothetical prote
1130	85.5	2.4	1281	2	JC5368	1203	85	2.4	1873	2	T30944	hypothetical prote
1131	85.5	2.4	1309	2	T13158	1204	85	2.4	2015	2	T30944	surface protein pr
1132	85.5	2.4	1436	2	UQ2294	1205	85	2.4	2470	2	T50726	hypothetical prote
1133	85.5	2.4	1458	2	A45665	1206	85	2.4	3328	2	T30835	cation-independent
1134	85.5	2.4	1460	2	S48457	1207	85	2.4	3430	1	GNMWV	breast cancer tumo
1135	85.5	2.4	1816	1	S68960	1208	85	2.4	3938	2	T42761	genome polypeptid
1136	85.5	2.4	3329	2	T30904	1209	84.5	2.4	229	2	C97030	Bassoon protein -
1137	85.5	2.4	6658	2	T13931	1210	84.5	2.4	322	2	B84635	arginase (imported
1138	85	2.4	128	2	T05635	1211	84.5	2.4	337	2	S42479	hypothetical prote
1139	85	2.4	192	2	S53591	1212	84.5	2.4	384	2	A70805	glyceroldehyde-3-p
1140	85	2.4	209	2	E87589	1213	84.5	2.4	396	2	T10951	probable lpxn prot
1141	85	2.4	238	2	T26419	1214	84.5	2.4	412	2	C72548	naringenin-chalcon
1142	85	2.4	319	2	B35090	1215	84.5	2.4	413	2	A55328	probable dihydroli
1143	85	2.4	339	2	G70915	1216	84.5	2.4	444	2	F86329	transcription fact
1144	85	2.4	376	2	S36247	1217	84.5	2.4	445	2	AH2480	hypothetical prote
1145	85	2.4	387	2	AC3618	1218	84.5	2.4	532	2	T49467	hypothetical prote
1146	85	2.4	397	2	A99907	1219	84.5	2.4	536	2	T17217	related to COP1-in
1147	85	2.4	408	2	B87436	1220	84.5	2.4	543	2	A41211	hypothetical prote
1148	85	2.4	413	2	T26040	1221	84.5	2.4	570	2	D97738	early growth respo
1149	85	2.4	418	2	T16713	1222	84.5	2.4	572	2	B46529	hypothetical prote
1150	85	2.4	442	2	DMECS	1223	84.5	2.4	572	2	S73901	Ig Y heavy chain (
1151	85	2.4	469	2	A83411	1224	84.5	2.4	600	2	E86854	ABC transporter y)
1152	85	2.4	474	2	S15921	1225	84.5	2.4	609	1	A42358	hypothetical prote
1153	85	2.4	482	2	AG1147	1226	84.5	2.4	609	2	G87496	vibriolysin (EC 3
1154	85	2.4	484	2	A41487	1227	84.5	2.4	616	2	T38473	peptidase, M23/M3
1155	85	2.4	511	1	UQ1935	1228	84.5	2.4	636	2	S63131	probable serine/th
1156	85	2.4	515	1	IQMCL	1229	84.5	2.4	658	2	S60170	probable membrane
1157	85	2.4	535	2	S65762	1230	84.5	2.4	662	2	T41442	protein kinase Pak
1158	85	2.4	539	2	S40900	1231	84.5	2.4	666	2	H75295	omnipotent nonsens
1159	85	2.4	540	2	JC4917	1232	84.5	2.4	697	2	T03834	transketolase - De
1160	85	2.4	548	1	A40449	1233	84.5	2.4	706	2	D84466	nuclear distributi
1161	85	2.4	572	1	VGNZBA	1234	84.5	2.4	719	2	T52510	hypothetical prote
1162	85	2.4	600	2	S07638	1235	84.5	2.4	729	2	E70803	hypothetical prote
1163	85	2.4	626	1	NBHUIA	1236	84.5	2.4	737	2	H95882	hypothetical prote
1164	85	2.4	626	2	S53871	1237	84.5	2.4	747	1	ORCPE	probable aldehyde
1165	85	2.4	646	2	SS6201	1238	84.5	2.4	755	2	T20950	ferrichrome-iron r
1166	85	2.4	673	2	S11840	1239	84.5	2.4	758	2	A10609	hypothetical prote
1167	85	2.4	689	2	A83036	1240	84.5	2.4	758	2	AB0167	ATP-dependent Clp
1168	85	2.4	693	2	C70167	1241	84.5	2.4	758	2	T31994	ATP-dependent Clp
1169	85	2.4	693	2	T19551	1242	84.5	2.4	775	2	F98136	hypothetical prote
1170	85	2.4	715	2	S76492	1243	84.5	2.4	786	2	T16509	hypothetical prote
1171	85	2.4	725	2	F81845	1244	84.5	2.4	821	2	AD1507	hypothetical prote
1172	85	2.4	747	2	T34329	1245	84.5	2.4	835	2	T34770	probable secreted
1173	85	2.4	750	2	S06726	1246	84.5	2.4	903	2	D87250	probable protein p
1174	85	2.4	750	2	F95039	1247	84.5	2.4	928	2	G86546	DNA mismatch repa
1175	85	2.4	750	2	H97909	1248	84.5	2.4	928	2	G81591	polymorphic oute
1176	85	2.4	751	2	F69338	1249	84.5	2.4	941	2	S78633	polymorphic membra
1177	85	2.4	781	2	S37032	1250	84.5	2.4	967	1	SYMTAT	isoleucine-tRNA li
1178	85	2.4	789	2	S44759	1251	84.5	2.4	967	1	SYMTAT	alanine-tRNA ligas
1179	85	2.4	841	2	S69563	1252	84.5	2.4	998	2	I41078	hemolysin - Escher
1180	85	2.4	859	2	B90768	1253	84.5	2.4	1018	2	AG0703	conserved hypochet
1181	85	2.4	907	2	A45560	1254	84.5	2.4	1021	2	T15765	hypothetical prote
1182	85	2.4	936	2	D97630	1255	84.5	2.4	1035	2	A64686	cation efflux syst
1183	85	2.4	946	1	IYHU2	1256	84.5	2.4	1055	2	D97225	carbamoylphosphate
1184	85	2.4	958	2	S45466	1257	84.5	2.4	1117	2	S63399	probable membrane
1185	85	2.4	970	2	E70533	1258	84.5	2.4	1133	2	A39962	kinase-related tra
1186	85	2.4	982	2	T34830	1259	84.5	2.4	1131	2	T15617	hypothetical prote
1187	85	2.4	1015	2	JC6552	1260	84.5	2.4	1148	2	AD0198	transcription-repa
1188	85	2.4	1059	2	E87058	1261	84.5	2.4	1148	2	F86403	probable transposo
1189	85	2.4	1091	2	A44147	1262	84.5	2.4	1150	2	S58775	mypl protein - smu
1190	85	2.4	1120	2	T01863	1263	84.5	2.4	1181	2	C86349	F8K7.4 protein - A
1191	85	2.4	1140	2	E70729	1264	84.5	2.4	1187	2	T31351	endo-1,4-beta-xyla
1192	85	2.4	1203	2	T01287	1265	84.5	2.4	1215	2	S50428	probable Ca2+-tran
1193	85	2.4	1217	2	T25894	1266	84.5	2.4	1216	2	T34101	hypothetical prote
1194	85	2.4	1246	2	AC2372	1267	84.5	2.4	1223	2	T15316	hypothetical prote
1195	85	2.4	1270	2	T30339	1268	84.5	2.4	1235	2	T16346	hypothetical prote
1196	85	2.4	1273	1	TDRRTT	1269	84.5	2.4	1442	2	T42607	transcription acti
1197	85	2.4	1274	2	E81779	1270	84.5	2.4	1468	2	A44345	nucleoprotein - rat
									1520	1	TVFPA	protein-tyrosine k

1271	84.5	2.4	1560	2	T02885	peroxisome prolifer	1344	84	2.4	1280	2	T00365	hypothetical prote
1272	84.5	2.4	1791	2	T02345	hypothetical prote	1345	84	2.4	1289	2	E90098	RNA polymerase III
1273	84.5	2.4	1819	2	D97033	uncharacterized pr	1346	84	2.4	1350	2	T30341	zinc finger protei
1274	84.5	2.4	2059	2	D82671	surface protein XP	1347	84	2.4	1401	2	T48079	hypothetical prote
1275	84.5	2.4	2130	2	AB0821	probable exported	1348	84	2.4	1430	2	T12449	hypothetical prote
1276	84.5	2.4	3149	1	Q0888	BRF1 protein - hu	1349	84	2.4	1518	2	S37928	probable purine nu
1277	84.5	2.4	3344	2	U01899	genome polyprotein	1350	84	2.4	1570	2	AC2012	hypothetical prote
1278	84	2.4	259	2	E69276	conserved hypochet	1351	84	2.4	1601	2	AB1730	hypothetical prote
1279	84	2.4	280	2	A84117	flagellar hook-bas	1352	84	2.4	1655	2	T32633	hypothetical prote
1280	84	2.4	317	2	S55316	mucin (clone PGM-2	1353	84	2.4	1829	2	T24583	hypothetical prote
1281	84	2.4	331	2	T15837	hypothetical prote	1354	84	2.4	2043	2	T18524	scavenger receptor
1282	84	2.4	341	2	T48858	acetylpolymine am	1355	84	2.4	2061	2	T13751	transcription fact
1283	84	2.4	346	2	A99173	hypothetical prote	1356	84	2.4	2430	1	A34971	protein-tyrosine-p
1284	84	2.4	347	2	H95406	conserved hypochet	1357	84	2.4	2523	2	F70846	probable ppe prote
1285	84	2.4	347	2	S10571	mucin 1 precursor,	1358	84	2.4	2630	2	T08868	polyprotein pi - A
1286	84	2.4	402	2	E86185	hypothetical prote	1359	84	2.4	3295	2	AE0074	probable adhesin Y
1287	84	2.4	416	2	A55237	transcription fact	1360	83.5	2.4	212	2	S71114	ribosomal protein
1288	84	2.4	437	2	S15306	CPP-4-keto-6-deoxy	1361	83.5	2.4	299	1	G69263	MJ1232 protein hom
1289	84	2.4	440	2	E71293	hypothetical prote	1362	83.5	2.4	302	2	A84062	ferrichrome ABC tr
1290	84	2.4	441	2	T31482	hypothetical prote	1363	83.5	2.4	335	2	S08341	myristylated alant
1291	84	2.4	448	2	A27631	cellulase (EC 3.2.	1364	83.5	2.4	341	1	DEJWG	glyceraldhyde-3-P
1292	84	2.4	473	1	A53036	Ca2+/calmodulin-de	1365	83.5	2.4	345	2	E88103	protein M10G11.5 l
1293	84	2.4	491	2	H84477	probable ptra-like	1366	83.5	2.4	361	2	E84678	probable carboxype
1294	84	2.4	491	2	F70659	probable pbpa prot	1367	83.5	2.4	398	2	A35281	integumentary muc
1295	84	2.4	496	2	S00855	hypothetical prote	1368	83.5	2.4	409	2	A44346	RAD23 protein homo
1296	84	2.4	502	2	T24227	hypothetical prote	1369	83.5	2.4	418	2	E90841	probable trehalase
1297	84	2.4	529	2	H84049	hypothetical prote	1370	83.5	2.4	428	2	EC5338	3-phosphoshikimate
1298	84	2.4	546	2	AG0586	phosphoglucumutase	1371	83.5	2.4	447	2	F82862	conjugal transfer
1299	84	2.4	549	2	A90253	hypothetical prote	1372	83.5	2.4	449	2	B86763	hypothetical prote
1300	84	2.4	563	2	T00359	pectin methylster	1373	83.5	2.4	450	2	C90608	hypothetical prote
1301	84	2.4	572	2	AC1200	phosphotransferase	1374	83.5	2.4	463	2	E70657	hypothetical prote
1302	84	2.4	572	2	A11557	phosphotransferase	1375	83.5	2.4	468	2	A70065	hypothetical prote
1303	84	2.4	584	2	T19061	hypothetical prote	1376	83.5	2.4	482	2	D85913	hypothetical prote
1304	84	2.4	597	2	T35746	hypothetical prote	1377	83.5	2.4	482	2	B91069	succinate-semialde
1305	84	2.4	607	2	T25922	hypothetical prote	1378	83.5	2.4	485	2	D85699	trehalase, peripla
1306	84	2.4	633	2	AH1598	acyltransferase (c	1379	83.5	2.4	489	2	E63959	2-isopropylmalate
1307	84	2.4	639	2	S70126	hypothetical prote	1380	83.5	2.4	502	2	T01996	nucleoid DNA-bind
1308	84	2.4	659	1	B44212	structural protein	1381	83.5	2.4	511	1	VGBB1K	glycoprotein C - h
1309	84	2.4	676	2	AE2417	hypothetical prote	1382	83.5	2.4	511	1	VGBB1K	glycoprotein C - h
1310	84	2.4	677	2	E70722	hypothetical prote	1383	83.5	2.4	518	2	T49778	hypothetical prote
1311	84	2.4	679	2	T52163	hypothetical prote	1384	83.5	2.4	519	1	JX0166	NADH oxidase (hydr
1312	84	2.4	695	2	E86627	cell division prot	1385	83.5	2.4	545	2	D87259	phosphoglucumutase
1313	84	2.4	695	2	S28533	lma protein - Lact	1386	83.5	2.4	556	2	UC5132	alpha-amylase (EC
1314	84	2.4	702	2	G01840	T-box protein 2 -	1387	83.5	2.4	565	2	S04782	alpha,alpha-trehal
1315	84	2.4	710	1	Q08E22	membrane antigen g	1388	83.5	2.4	582	2	T07952	lectin-like protei
1316	84	2.4	712	2	G91280	aerobic ribonuci	1389	83.5	2.4	601	2	T37738	hypothetical prote
1317	84	2.4	712	2	G86121	anaerobic ribonuci	1390	83.5	2.4	601	2	JC4576	serine proteinase
1318	84	2.4	727	2	A88131	protein P10G7.9 [i	1391	83.5	2.4	616	2	C75588	conserved hypochet
1319	84	2.4	732	2	S47688	cd2+-exporting ATP	1392	83.5	2.4	617	2	T16189	hypothetical prote
1320	84	2.4	814	2	A71419	probable allene ox	1393	83.5	2.4	630	2	A81903	probable chapone
1321	84	2.4	820	2	B72575	hypothetical prote	1394	83.5	2.4	633	2	S62057	proline-rich prote
1322	84	2.4	823	2	C81835	probable P-type ca	1395	83.5	2.4	638	1	C69126	ferrous iron trans
1323	84	2.4	823	2	D81129	cation transport A	1396	83.5	2.4	638	1	XXAV	dihydroliopamide S
1324	84	2.4	827	2	F72414	ribonucleotide red	1397	83.5	2.4	647	2	D85359	hypothetical prote
1325	84	2.4	832	2	AE1452	hypothetical prote	1398	83.5	2.4	647	2	T41121	heat shock protein
1326	84	2.4	834	2	T42702	hypothetical prote	1399	83.5	2.4	668	2	T26724	hypothetical prote
1327	84	2.4	851	2	S67285	NMD1 protein - yea	1400	83.5	2.4	682	2	A42121	transcription fact
1328	84	2.4	865	2	T41685	probable gamma-act	1401	83.5	2.4	694	2	S68442	Grb2-associated bi
1329	84	2.4	866	2	D44234	fibrinogen alpha c	1402	83.5	2.4	712	1	S69782	outer membrane pro
1330	84	2.4	876	2	T49801	hypothetical prote	1403	83.5	2.4	714	2	D87179	probable fatty oxi
1331	84	2.4	878	2	AH2075	ferrichrome-iron r	1404	83.5	2.4	728	2	T26607	hypothetical prote
1332	84	2.4	897	1	A39255	cytokine receptor	1405	83.5	2.4	752	1	C2HU	complement C2 prec
1333	84	2.4	935	2	E84491	hypothetical prote	1406	83.5	2.4	756	2	E82236	ATP-dependent Clp
1334	84	2.4	940	2	D89723	protein F39D8.1b l	1407	83.5	2.4	759	2	D84301	cell division cycl
1335	84	2.4	945	2	T21998	hypothetical prote	1408	83.5	2.4	762	2	H87466	beta-D-glucosidase
1336	84	2.4	1026	2	AE0671	probable RND-famil	1409	83.5	2.4	793	2	S34830	kinasin-related pr
1337	84	2.4	1041	2	S55862	probable membrane	1410	83.5	2.4	809	2	T41645	probable spindie p
1338	84	2.4	1042	2	T29307	hypothetical prote	1411	83.5	2.4	824	2	T23096	hypothetical prote
1339	84	2.4	1070	2	C75506	hypothetical prote	1412	83.5	2.4	851	2	D87252	tonB-dependent rec
1340	84	2.4	1171	2	T42372	probable guanilate	1413	83.5	2.4	852	2	C98310	haas protein (Y089
1341	84	2.4	1192	2	T08609	hypothetical prote	1414	83.5	2.4	870	2	T30110	hypothetical prote
1342	84	2.4	1219	2	S54570	probable membrane	1415	83.5	2.4	886	2	A82825	aconitate hydratase
1343	84	2.4	1271	2	D64237	hypothetical prote	1416	83.5	2.4	898	2	T26577	hypothetical prote

1417	83.5	2.4	923	2	AH2972	heme receptor hasr
1418	83.5	2.4	938	1	QOBE24	nuclear antigen EB
1419	83.5	2.4	989	2	T47503	hypothetical prote
1420	83.5	2.4	989	2	T01519	hypothetical prote
1421	83.5	2.4	1003	2	C71139	hypothetical prote
1422	83.5	2.4	1013	2	G71460	probable outer mem
1423	83.5	2.4	1014	2	T13476	hypothetical prote
1424	83.5	2.4	1016	2	S30236	genome polypotein
1425	83.5	2.4	1062	2	B26330	hypothetical prote
1426	83.5	2.4	1063	2	T03743	bifocal protein -
1427	83.5	2.4	1065	2	S19482	hypothetical prote
1428	83.5	2.4	1179	2	T04488	DNA topoisomerase
1429	83.5	2.4	1215	2	T00364	hypothetical prote
1430	83.5	2.4	1230	2	T07663	soluble starch syn
1431	83.5	2.4	1232	2	B39432	ATP-dependent deox
1432	83.5	2.4	1244	2	T19068	hypothetical prote
1433	83.5	2.4	1255	2	T31065	diaphanous protein
1434	83.5	2.4	1292	2	T31462	probable magnesium
1435	83.5	2.4	1312	2	B35006	beta-N-acetylhexos
1436	83.5	2.4	1320	2	JC5630	TCOP1 protein - mo
1437	83.5	2.4	1329	2	C69048	cobalamin gamma-1 ch
1438	83.5	2.4	1607	1	MMMSB2	IgA-specific metal
1439	83.5	2.4	1694	2	H64106	IgA-specific metal
1440	83.5	2.4	1702	2	A41859	zinc finger protei
1441	83.5	2.4	1706	2	B84459	lysin-specific cy
1442	83.5	2.4	1732	2	T30836	microtubule-associ
1443	83.5	2.4	1824	1	ORHUMT	protein-tyrosine-p
1444	83.5	2.4	2450	2	S71625	probable histidine
1445	83.5	2.4	2471	2	T03820	adenomalous polyo
1446	83.5	2.4	2845	2	T19505	DNA-directed DNA p
1447	83.5	2.4	3122	2	T17202	breast cancer susc
1448	83.5	2.4	3329	2	S25111	alpha-2-macroglobu
1449	83.5	2.4	4545	1	DS5111	alcohol dehydrogen
1450	83	2.4	285	2	D69835	glyceraledehyde-3-p
1451	83	2.4	340	2	T09663	hypothetical prote
1452	83	2.4	340	2	T28080	T-cell surface gly
1453	83	2.4	351	1	RWHUC2	hypothetical prote
1454	83	2.4	372	2	T21757	hypothetical prote
1455	83	2.4	376	2	T39138	hypothetical prote
1456	83	2.4	386	2	S45569	nuclear factor I-A
1457	83	2.4	390	1	QOBE77	glycoprotein I pre
1458	83	2.4	400	2	C75336	serine proteinase,
1459	83	2.4	414	2	A12544	hypothetical prote
1460	83	2.4	440	2	T86698	hypothetical prote
1461	83	2.4	445	2	S00256	Krox-20 protein -
1462	83	2.4	450	2	S73419	signal recognition
1463	83	2.4	451	1	S68455	serine/threonine-s
1464	83	2.4	452	2	C97162	UDP-N-acetylmuram
1465	83	2.4	470	2	D84863	hypothetical prote
1466	83	2.4	482	2	T22981	hypothetical prote
1467	83	2.4	487	2	PQ0259	hypothetical prote
1468	83	2.4	495	2	C83598	hypothetical prote
1469	83	2.4	524	2	E96572	protein F12M16.10
1470	83	2.4	534	2	G75472	GTP-binding protei
1471	83	2.4	546	2	G85568	phosphoglucosylase
1472	83	2.4	546	2	G90718	phosphoglucosylase
1473	83	2.4	553	2	I37417	glycerol kinase -
1474	83	2.4	553	2	C75318	hypothetical prote
1475	83	2.4	561	2	B83754	arginine-tRNA liga
1476	83	2.4	567	2	T16625	asparagine synthas
1477	83	2.4	578	2	G82950	conserved hypotet
1478	83	2.4	587	2	A56015	finger protein SIG
1479	83	2.4	589	2	G69815	ABC transporter (A
1480	83	2.4	593	2	JC4175	acid phosphatase (
1481	83	2.4	603	2	A82753	dihydrolipomide d
1482	83	2.4	638	2	H82630	hypothetical prote
1483	83	2.4	650	2	A82004	hypothetical prote
1484	83	2.4	677	2	T39713	zinc finger protei
1485	83	2.4	690	2	H86464	hypothetical prote
1486	83	2.4	703	2	T24975	hypothetical prote
1487	83	2.4	705	2	T30521	surface protein -
1488	83	2.4	706	2	E30411	synapsin Ia - Dovi
1489	83	2.4	707	2	A46691	E-box-binding prot

1490	83	2.4	708	1	M2XR1L	structural protein
1491	83	2.4	708	1	M2XR2J	structural protein
1492	83	2.4	712	1	A47331	ribonucleoside-tri
1493	83	2.4	722	2	T22359	hypothetical prote
1494	83	2.4	728	2	F72693	probable phosphoe
1495	83	2.4	729	2	T51896	probable translati
1496	83	2.4	738	2	T40035	hypothetical prote
1497	83	2.4	803	2	A86655	hypothetical prote
1498	83	2.4	843	2	A87275	trans-dependent rec
1499	83	2.4	846	2	S52418	GMP-binding regula
1500	83	2.4	854	1	XYBT1	protein N-acetyltr

## ALIGNMENTS

RESULT 1  
A40020 collagen alpha 1(XII) chain precursor - chicken  
N:Alternate names: fibrochimerin  
C:Species: Gallus gallus (chicken)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004  
C:Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811  
R:Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Niehida, Y.; Obar  
J. Cell Biol. 115, 209-221, 1991  
A:Title: The complete primary structure of type XII collagen shows a chimeric molecule w  
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.  
A:Reference number: A40020; MUID:92011862; PMID:1918137  
A:Accession: A40020  
A:Molecule type: mRNA  
A:Residues: 1-3124 <YMS>  
A:Cross-references: UNIPARC:P13944; UNIPARC:UPI0000126D2D; GB:D00824; NID:9222810; PIDN:  
A:Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,  
R:Gordon, M.K.; Gerecke, D.R.; Dubler, B.; van der Rest, M.; Olsen, B.R.  
J. Biol. Chem. 264, 19772-19778, 1989  
A:Title: Type XII collagen. A large multidomain molecule with partial homology to type I.  
A:Reference number: A34485; MUID:90062079; PMID:2584192  
A:Accession: A34485  
A:Molecule type: mRNA  
A:Residues: 2456-2758 'A', 2760-2802 'F', 2804-2976 'F', 2978-3124 <GOR>  
A:Cross-references: UNIPARC:UPI000011233; EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PI  
A:Accession: B34485  
A:Molecule type: protein  
A:Residues: 2772-2792;2846-2873 <GOR2>  
A:Cross-references: UNIPARC:UPI0000173C3F; UNIPARC:UPI0000173C40  
R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987  
A:Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c  
A:Reference number: A28037; MUID:87317590; PMID:3476925  
A:Accession: A28037  
A:Molecule type: mRNA  
A:Residues: 2860-2976 'F', 2978-3074 'AG', <GOR3>  
A:Cross-references: UNIPARC:UPI0000112F4; EMBL:M17375; NID:9211649; PIDN:AAA48718.1; PI  
A:Note: this sequence has been revised in reference A34485  
R:Koch, M.; Bernasconi, C.; Chiquet, M.  
Eur. J. Biochem. 207, 847-856, 1992  
A:Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of  
A:Reference number: S23814; MUID:92362621; PMID:11233460  
A:Accession: S23814  
A:Molecule type: protein  
A:Residues: 'X', '1333', 'Q', '1335-1347', '1914-1928', '2504', 'X', '2506', 'X', '2508-2511', 'X', '2513-2517' <  
A:Cross-references: UNIPARC:UPI0000173C41; UNIPARC:UPI0000173C42; UNIPARC:UPI0000173C43  
R:Dubler, B.; van der Rest, M.  
J. Biol. Chem. 262, 17724-17727, 1987  
A:Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of peptin-  
A:Reference number: S22254; MUID:88087065; PMID:3121603  
A:Accession: S22254  
A:Molecule type: protein  
A:Residues: 2831-2832, 'T', 2834, 'R', 2836-2843;3002-3014 <DUB>  
A:Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45  
R:Trueb, J.; Trueb, B.  
Biochim. Biophys. Acta 1171, 97-98, 1992  
A:Title: The two splice variants of collagen XII share a common 5' end.

[illegible]

Db 416 TIMEKTQGVK-----:QVECSRGVDVAKADVVELFDVSGYSIGIANVVKRAFLVELVKS 468

Qy 525 FEISDTDRIGAVOTTYEORLEFEGFDKSSKPDILNAIKRVGVWSGSTGAINFALQ 584

Db 469 FEISPRKVOISLVQVSRDHEMFESLNRYNRVKDIIQAINTEFPFGSGSTNGKAMTYREK 528

Qy 585 LF---KSKSPNKRKMILITIDGRSYDDVIRIPMAAHLKGVITAYIQAAMAQEELEVIAT 641

Db 529 VFTVTSKSGRPNVPRWMLITIDGKSSDAFKEPALKKMDADVEIRAVGVKDAVTELEAIAS 588

Qy 642 HPARDHSFFVDEFDNLHQYVPRRIQNICTEPNSQ 675

Db 589 PPAETHVYTVDEFDFAFORISFELTOSVCLRIEOE 622

RESULT 2

A37797

collagen alpha 3(VI) chain precursor - chicken

C|Species: Gallus gallus (chicken)

C|Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 16-Aug-2004

C|Accession: A37797; A34270; A32674

R|Doliana, R.; Bonaldo, P.; Colombatti, A.

J|Cell Biol. 111, 2197-2205, 1990

A|Title: Multiple forms of chicken alpha3(VI) collagen chain generated by alternative splicing

A|Reference number: A37797; PMID:1977751

A|Accession: A37797

A|Molecule type: mRNA

A|Residues: 1-253;112-321;434-453;504-518;635-655;704-717;832-853 <DOL>

A|Cross-references: UNIPROT: P15999; UNIPARC:UPI0000173C31; UNIPARC:UPI0000173C32; UNIPARC:UPI0000173C33; UNIPARC:UPI0000173C34; UNIPARC:UPI0000173C35

R|Bonaldo, P.; Russo, V.; Buccicotti, F.; Doliana, R.; Colombatti, A.

Biochemistry 29, 1245-1254, 1990

A|Title: Structural and functional features of the alpha3 chain indicate a bridging role

A|Reference number: A34270; PMID:90212613; PMID:2322559

A|Accession: A34270

A|Molecule type: mRNA

A|Residues: 224-2871 <BON>

A|Cross-references: UNIPARC:UPI0000173C38; GB:M24282

A|Note: The authors translated the codon TTC for residue 1916 as Leu and TTC for residue 1917 as Phe.

J|Biol. Chem. 264, 20235-20239, 1989

A|Title: The carboxyl termini of the chicken alpha3 chain of collagen VI is a unique motif

A|Reference number: A32674; PMID:90062147; PMID:2584214

A|Accession: A32674

A|Molecule type: mRNA

A|Residues: 2151-2199; 2792-3137 <BO2>

A|Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI0000173C3A; GB:M24282

C|Genetics:

A|Introns: 30/1; 236/1; 437/1; 638/1; 838/1

C|Superfamily: collagen VII

C|Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracellular matrix

F|1-25/Domain: signal sequence #status predicted <SIG>

F|26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT>

F|26-2042/Domain: non-collagenous #status predicted <NNC>

F|36-202/Domain: von Willebrand factor type A repeat homology <VM01>

F|239-404/Domain: von Willebrand factor type A repeat homology <VM02>

F|442-607/Domain: von Willebrand factor type A repeat homology <VM03>

F|642-807/Domain: von Willebrand factor type A repeat homology <VM04>

F|840-1004/Domain: von Willebrand factor type A repeat homology <VM05>

F|1033-1197/Domain: von Willebrand factor type A repeat homology <VM06>

F|1237-1400/Domain: von Willebrand factor type A repeat homology <VM07>

F|1439-1604/Domain: von Willebrand factor type A repeat homology <VM08>

F|1639-1804/Domain: von Willebrand factor type A repeat homology <VM09>

F|1838-2010/Domain: von Willebrand factor type A repeat homology <VM10>

F|2043-2378/Domain: collagenous #status predicted <COL>

F|2045-2047/Region: cell attachment (R-G-D) motif

F|2153-2155/Region: cell attachment (R-G-D) motif

F|2159-2161/Region: cell attachment (R-G-D) motif

F|2379-3137/Domain: non-collagenous #status predicted <NC>

F|2405-2577/Domain: von Willebrand factor type A repeat homology <VM11>

F|2623-2806/Domain: von Willebrand factor type A repeat homology <VM12>

F|2803-2846/Domain: platelet glycoprotein Ib-like #status predicted <GPI>

F:2954-1039/Domain: fibronectin type III repeat homology <FN3>  
 F:3072-3122/Domain: animal knitz-type proteinase inhibitor homology <BPI>  
 F:201,2084,2436,2563,2581,2687,2920,3003/Binding site: carbohydrate (asn) (covalent

Query Match 14.4% Score 504.5; DB 2; Length 3117;  
 Best Local Similarity 30.7%; Pred. No. 8,9e-25;  
 Matches 121; Conservative 87; Mismatches 155; Indels 31; Gaps 8;

QY 293 DLSFLIDGSTSIGKRRFRIOQLADVAQALDIGPAGLMGVGYGDNPAHFKHTN 352  
 Db 38 DIFLVDSMSIGKEHFQVREFLVDYKALDVGNDPRFALVQSGNPHFQNTYPS 97  
 QY 353 SRDLTAIEKITTQGGLSNVGRALSFTYKNFFSKANGRS--GAPVVVVAVDGPMDKY 410  
 Db 98 NQDVLSTANMPYWGSGSKTGKLEYLENHLTKAAGRSAGEVQVYIVLTDGSGDDV 157  
 QY 411 EEAARLARESGINIFITIEGAENEKQYVVEPNANAVORTNGFSLHVSFGLHKT 470  
 Db 158 ALPSSVLKSAHVMIAVVQDAVEGELKEIASRPDT-----HIFNLENTALHGI 208  
 QY 471 LQPLVK--RVCDTDLRLACSK-----TCINSGADIGFVIDGSSVGTGNFTVLQFVTNLT 522  
 Db 209 VGDVLASVRTSMTEQAGAKGLVMDITQESADILFLDSSDNGSVAFQAIRFIVNLI 268  
 QY 523 KEFEISTDTIRIGAVQYTYEORLEFGFDKYSKPDILNAIKRVGYWSG-GTSTGAALNFA 581  
 Db 269 ESLRVGAQOIHIGVQVSDQPRTEFALNSYSTKADVLDAVKALSFPGCKEANTGALEYV 328  
 QY 582 LEOLFKKSPKPK-----RKLMLITDGRSYDDVRIPMAAHLKGVITYAIGVAAQEELE 636  
 Db 329 VENLFTQGGSRIEBAVQIIVLISGESSDDIREGLAIVKQASISFSGIVLNASAEI 388  
 QY 637 EVIATHPARDSFEVDEFD--NLHQVPRIIQNI 668  
 Db 389 QQIAT----DGSFAFTALDIRNLALRELLPNI 418

## RESULT 3

A337979  
 cartilage matrix protein precursor - human  
 C/Species: Homo sapiens (man)  
 C/Date: 12-Jul-1991 #sequence\_revision 12-Jul-1991 #text\_change 09-Jul-2004  
 C/Accession: A37979; B37979  
 R/Junkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; SH  
 J. Biol. Chem. 265, 19624-19631, 1990  
 A/Title: Structure and chromosomal location of the human gene encoding cartilage matrix  
 A/Reference number: A37979; MUID:91060568; PMID:2246248  
 A/Accession: A37979

A/Molecule type: DNA  
 A/Status: preliminary  
 A/Residues: 1-496 <JEN>  
 A/Cross-references: UNIPROT:P21941; UNIPARC:UPI000004F1ED; GB:J05667  
 A/Accession: B37979  
 A/Molecule type: mRNA  
 A/Residues: 157-290, 'L', 292-496 <JE2>  
 A/Cross-references: UNIPARC:UPI000016A6E8; GB:M55683; GB:J05666; GB:J05667; NID:9180651;  
 C/Genetics:

A/Gene: GDB:CRM  
 A/Cross-references: GDB:127280; OMIM:115437  
 A/Map position: 1p35-1p35  
 A/Intons: 32/1, 147/3, 222/1, 264/1, 403/1, 454/1, 481/1  
 C/Complex: homotrimer  
 C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe  
 C/Keywords: glycoprotein; homotrimer  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-496/Product: cartilage matrix protein #status predicted <MAT>  
 F:39-206/Domain: von Willebrand factor type A repeat homology <VWA1>  
 F:227-262/Domain: EGF homology <EGF>  
 F:273-437/Domain: von Willebrand factor type A repeat homology <VMA2>  
 F:76,344/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:221-238,234-247,249-263/Disulfide bonds: #status predicted

Query Match 14.3% Score 501.5; DB 2; Length 496;  
 Best Local Similarity 28.8%; Pred. No. 8.9e-26;

Matches 129; Conservative 80; Mismatches 178; Indels 61; Gaps 9;

QY 273 EELSTQSLFVSLGDPNCK--IDLSPIDGSTSIGKRRFRIOQLADVAQALDIGPAG 329  
 Db 19 QALCSPELAQOSRGH-LCTRPRPDLVFRVDSNSVREVEKVKVFLSQVIESLDVGN 77  
 QY 330 PLMGVOYGDNPATHEFLKHTNSRDILKTAIEKITQGGLSNVGRALSFTYKNFFSKANG 389  
 Db 78 TRVGMVYASTVXQEFSLRAHVSKAALQAVRRIQPLSTGTMTGLAIFATKAFDAEG 137  
 QY 390 NRSAPR---VVVVMDVGTLDVEEASRLARESGINIFITIEGAENE--KQYVEPN 444  
 Db 138 GRKSPDISKRVVIVYVDGRQDVSQVDSAPARASGVELFAIGV-GSDVKAATLRQIASEPQ 196  
 QY 445 FANKAVRTNGFYSLHVSFGLHKTLP-----LVKRCVDTDLRLACSKTCINLS----- 493  
 Db 197 DEHYD-----YVESISVIEKLSRKQEAFCVSDLCATGDHCQVCISSPSSTY 246  
 QY 494 -----ADIGFVIDGSSVGTGNFTVLQFVTNLTKEFE 526  
 Db 247 CACHGEFTLNSDKTCNVCSGGGSSATDVLFLIDGSKSVRPNFELVKKFISQIVDTLD 306  
 QY 527 ISPTDIRIGAVQYTYEORLEFGFDKYSKPDILNAIKRVGYWSGSGTGAALNFALEQLF 586  
 Db 307 VSDKLAQVGLVQYSSVRQEPFLGRFHTKDIKAAVANNMSEMERGTWTGAALXYLIDNSF 366  
 QY 587 KKS--KPNRKMLITDGRSYDDVRIPMAAHLKGVITYAIGVAAQEELEVIATHP 643  
 Db 367 TVSSGARPGQKIGVFTDGRSODYINDAKKAKDLGFKFAVGVNAVEDELREIASEP 426  
 QY 644 ARDHSFEVDEFDNLHQVPRIIQNICTE 671  
 Db 427 VAHVFYTADEFKTINGKTLQKKICVE 454

## RESULT 4

A33809  
 cartilage matrix protein precursor - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 09-Jul-2004  
 C/Accession: A33809; A26364  
 R/Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Meubust, K.A.; Primmerger, E.; Arg  
 J. Biol. Chem. 264, 8126-8134, 1989  
 A/Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex  
 grins, Von Willebrand factor, complement factors B and C2, and epidermal growth factor.  
 A/Reference number: A33809; MUID:89255246; PMID:2542265  
 A/Accession: A33809

A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-493 <KIS>  
 A/Cross-references: UNIPROT:P05099; UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347; GB:X123  
 R/Argaves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetlinck, P.F.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987  
 A/Title: Structural features of cartilage matrix protein deduced from cDNA.  
 A/Reference number: A26364; MUID:87092429; PMID:3025875  
 A/Accession: A26364

A/Molecule type: mRNA  
 A/Residues: 78-493 <ARG>  
 A/Cross-references: UNIPARC:UPI000004F1EF; GB:M14792; NID:9211545; PIDN:AAA48695.1; PID:  
 C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe  
 F:37-204/Domain: von Willebrand factor type A repeat homology <VMA1>  
 F:225-260/Domain: EGF homology <EGF>  
 F:270-434/Domain: von Willebrand factor type A repeat homology <VMA2>

Query Match 14.0% Score 490; DB 2; Length 493;  
 Best Local Similarity 29.6%; Pred. No. 5.2e-25;  
 Matches 125; Conservative 68; Mismatches 177; Indels 52; Gaps 7;

QY 293 DLSFLIDGSTSIGKRRFRIOQLADVAQALDIGPAGLMGVGYGDNPAHFKHTN 352  
 Db 39 DLFVFIIDSSRSVRPQFEKVKVFLSVIEGLDVGPRSTRVGINVMSAKNGESLKHQT 98  
 QY 353 SRDLTAIEKITQGGLSNVGRALSFTYKNFFSKANGRSAPN---VVVVMDVGTLDK 409

```

Db      99 KAEILQAVQRIEPLSTGTMTGLAIQFAISRAFSPTDEGARLSPINKVAIVTDGRPDG 158
Qy      410 VEEASRIARSSGINIFP-----TIGAAENENQYVEENFANK---AV 450
Db      159 VQDSARARQAGLEIFAIGVRDMHTLRLQIASPELDDHVDVYESVIEKLTHTKFOEAR 218
Qy      451 C-----RTNGFYSLHVQSWFGIAHKTLOPLVGRVVDTRLACSKTCLN 492
Db      219 CVVSDLCATGDHDEQICISTPGSYKCAKCEGFLTND-----GKTS-----ACSGSGS 269
Qy      493 SADIGFVIDSSSVGTGNFRTVLOFTNLKEFEISDTDRIGAVQYTYEQRLFEGDKY 552
Db      270 ALDLVFLIDGSKSVRPENFELVKKFNIQIVESLEVESEKQAVGVQYSSSVROEFLPGQF 329
Qy      553 SSKRDLINAIKRVGWSGSGTGAINPALEQLF---KKSPPNKRKMLILITGRSYDDV 609
Db      330 KKKKDIKAAVKKAAVMEKGTWTGALKYLVDSFSISANGAPGVKGVIFTDSDYI 389
Qy      610 RIPMAAHLKGVITYAIGVMAAOEELVIAHPARDHSEFVDFDNLHOYVPRITONIC 669
Db      390 TDAKAKKADIGFRNFAVGVGAVIDELREIASEVVAHYFTADFRITISNGKKLQMKIC 449
Qy      670 TE 671
Db      450 VE 451

```

## RESULT 5

```

S66522
cartilage matrix protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66522
R/Author: A.; Hauser, N.; Studer, D.; Paulsson, M.; Haripi, L.; Boese, Z.
E/Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c
A/Reference number: S66522; MUID:96270751; PMID:8665920
A/Accession: S66522
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-500 <AS2>
A/References: UNIPROT:P51942; UNIPARC:UPI0000029480; EMBL:U35035; NID:g1163178; PI
C/Genetics:
A/Gene: CMP
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-500/Product: cartilage matrix protein #status predicted <MAT>
F:43-210/Domain: von Willebrand factor type A repeat homology <VWA1>
F:231-266/Domain: EGF homology <EGF>
F:277-441/Domain: von Willebrand factor type A repeat homology <VWA2>

```

```

Query March 14.0% Score 490; DB 2; Length 500;
Best Local Similarity 28.8%; Pred. No. 5.3e-25;
Matches 130; Conservative 72; Mismatches 184; Indels 66; Gaps 8;

Qy      266 SLGLVPEEELSTQSLPEVSLDPPNCKIDLSFLIDGSTSIGKRRPRIKOLADVAQAADI 325
Db      27 SLGLVPEEELSTQSLPEVSLDPPNCKIDLSFLIDGSTSIGKRRPRIKOLADVAQAADI 325
Qy      326 GPAGPLMGVOYQGNPATEHNLKTHNSRDLKTIKLTORGGISNNGRAISFTTKPFS 385
Db      326 GPAGPLMGVOYQGNPATEHNLKTHNSRDLKTIKLTORGGISNNGRAISFTTKPFS 385
Qy      78 GPNAITRGLVNVASTVKEPFLRAHSGKASLQAVRRIOPLSTGTMTGLAQFAITVALS 137
Db      78 GPNAITRGLVNVASTVKEPFLRAHSGKASLQAVRRIOPLSTGTMTGLAQFAITVALS 137
Qy      386 KANGNRSGAPN---VVVVMDVGMPTDKVEASRLARSSGINIFITTEGAENEN---KQYV 440
Db      138 DABGGRARSPISKVIVVTDGRQDSVRDVSEPARASGLELFAIGL-GRVDAKTLRQIA 196
Qy      441 VEPNFAKAVCRITNGFYSLHVQSWFGIAHKTLOP-----LVKRVCDTRLACSKTCLNS 493
Db      197 SEPDEHDV-----YESINVLIEKLAKKQGEAFVSDICATGHDHCEGLCVSSP 246
Qy      494 -----ADIGFVIDSSSVGTGNFRTVLOFTNL 522

```

```

Db      247 GSYTCACHBGFLLNSDGKTCNCRGGSSGASATDLVFLIDGSKSVRPENELVKKFNIQIV 306
Qy      523 KEFEISDTDRIGAVQYTYEQRLFEGDKYSSPDILNMIKRVYSGSGTGAINFLP 582
Db      307 DTLVDSDRLAQVGLVQYSSIROEPLGRFHSKDDIKAVRNMSYVEKGTMTGAALKYLI 366
Qy      583 EQLFKS---KPKRKRLMLITDGRSYDDVRIPMAAHLKGVITYAIGVMAAOEELVY 639
Db      367 DNFFTVSSGARPAQAGVIGVIFTDGRSDYINDAARAKOLGFRMFAVGVGNVDEELREI 426
Qy      640 AHPARDHSEFVDFDNLHOYVPRITONICTE 671
Db      427 ASEPVADHYFTADFRITISNGKKLQMKICVE 458

```

## RESULT 6

```

CGH03A
collagen alpha 3(VI) chain precursor [validated] - human
N/Contains: collagen alpha 3(VI) chain, splice form A9/N10(-)
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence_revision 12-Nov-1999 #text_change 16-Aug-2004
C/Accession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848; S26510; S48.
R/Chu, M.L.
submitted to GenBank, May 1998
A/Reference number: A59140
A/Accession: A59140
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-3176 <CHU>
A/References: UNIPROT:P12111; UNIPARC:UPI0000126DAF; GB:X52022; NID:g3127925; PIDN:
R/Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; Kuo, H.-J.; Glanville, R.; Maye
EMBO J. 9, 385-393, 1990
A/Title: Mosaic structure of globular domains in the human type VI collagen alpha-3 chain
itors.
A/Reference number: S13679; MUID:90151612; PMID:1689238
A/Accession: S13679
A/Molecule type: mRNA
A/Residues: 1-30,237-313, 'CW', 318-322, 'AR', 326-1815, 'FD', 1818-1819, 'ID', 1822-3176 <CH5>
A/Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:g3127925
A/Accession: S24465
A/Molecule type: protein
A/Residues: 574-585;965-973, 'X', 975-976;1306-1325;1361-1377;1381-1401;1473-1506, 'X', 1508-
-1962, 'X', 1964-1965;2018-2037;2374-2410;2445-2459;2466-2469, 'X', 2471-2474;2504-2508, 'X', ;
A/Cross-references: UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17;
CIC, UNIPARC:UPI0000173C1D; UNIPARC:UPI0000173C1E; UNIPARC:UPI0000173C1F; UNIPARC:UPI0000
10000173C25; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C27
R/Zanussi, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A/Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain s
A/Reference number: S28776; MUID:93054780; PMID:1339440
A/Accession: A57083
A/Molecule type: DNA
A/Residues: 310-328 <ZAN>
A/Cross-references: UNIPARC:UPI0000173C28
A/Accession: S28776
A/Molecule type: mRNA
A/Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZAN>
A/Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1; PID:5
R/Chu, M.L.; Mann, K.; Deutzmann, R.; Pithula-Conway, D.; Hsu-Chen, C.C.; Bernard, M.P.;
Eur. J. Biochem. 168, 309-317, 1987
A/Title: Characterization of three constituent chains of collagen type VI by peptide seq
A/Reference number: S00126; MUID:88029444; PMID:3665927
A/Accession: S00126
A/Molecule type: mRNA; protein
A/Residues: 2024-2046;2092-2156, 'R', 2203-2208, 'X', 2210-2211, 'X', 2213-2227;2228-2251;2234-
A/Cross-references: UNIPARC:UPI00001A705; UNIPARC:UPI0000173C29; UNIPARC:UPI0000173C2A;
ID:91335034
A/Note: the mRNA portion of the sequence corresponds to residues 2092-2157
R/Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Timpi, R.
J. Biol. Chem. 263, 18601-18606, 1988
A/Title: Amino acid sequence of the triple-helical domain of human collagen type VI.
A/Reference number: A31952; MUID:89066644; PMID:3198591

```

A:Accession: C31952  
 A:Molecule type: mRNA  
 A:Residues: 2038-2373 <CH4>  
 A:Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778  
 A:Note: parts of this sequence were determined by protein sequencing  
 R.Well, D.; Mattei, M.G.; Passage, E.; Van Cong, N.; Pribula-Conway, D.; Mann, K.; Deutz  
 Am. J. Hum. Genet. 42, 435-445, 1988  
 A:Title: Cloning and chromosomal localization of human genes encoding the three chains of  
 A:Reference number: A29848; MUID:88161046; PMID:3348212  
 A:Accession: C29848  
 A:Molecule type: mRNA  
 A:Residues: 2092-2151 <WE1>  
 A:Cross-references: UNIPARC:UPI000016A720; GB:M27449; NID:G291919; PIDN:AA52057.1; PID:  
 A:Note: part of this sequence was determined by protein sequencing  
 R.Jander, R.; Rautenberg, J.; Gnanville, R.W.  
 Eur. J. Biochem. 133, 39-46, 1983  
 A:Title: Further characterization of the three polypeptide chains of bovine and human sh  
 A:Reference number: 826506; MUID:83209648; PMID:685203  
 A:Accession: 826510  
 A:Molecule type: protein  
 A:Residues: 'SAIAGVAGV' <JAN>  
 A:Cross-references: UNIPARC:UPI0000173C2F  
 A:Note: this sequence cannot be reliably placed and probably represents the results from  
 R.Mayer, U.; Boeschl, E.; Nisch, R.; Specks, U.; Pan, T.C.; Chu, M.L.; Timpl, R.  
 Eur. J. Biochem. 225, 573-580, 1994  
 A:Title: Recombinant expression and properties of the Kunitz-type protease-inhibitor mod  
 A:Reference number: 548709; MUID:95045506; PMID:7525281  
 A:Accession: 548709  
 A:Molecule type: mRNA  
 A:Residues: 'MAMIFLITACGALAA', 3102-3176 <MAY>  
 A:Cross-references: UNIPARC:UPI0000173C30  
 A:Note: engineered sequence to allow isolation of the Kunitz-type proteinase inhibitor h  
 R.Arroux, B.; Merigau, K.; Saludjian, P.; Norris, F.; Norris, K.; Bjorn, S.; Olsen, O.;  
 submitted to the Brookhaven Protein Data Bank, August 1994  
 A:Reference number: A52812; PDB:1KNT  
 A:Contents: annotation, X-ray crystallography, 1.6 angstroms, residues 3106-3160  
 A:Note: engineered sequence expressed in Saccharomyces cerevisiae strain mt-663  
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit  
 sines are 5-hydroxylated and subsequently O-glycosylated.  
 C:Comment: The fibronectin type III repeat homology domain may be released during proces  
 C:Genetics:  
 A:Gene: GDB:COL6A3  
 A:Cross-references: GDB:119066; OMIM:120250  
 A:Map position: 2937.3-2937.3  
 C:Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGH1JA),  
 sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).  
 C:Function:  
 A:Description: structural component of extracellular tissue microfibrils associated with  
 C:Superfamily: collagen VI  
 C:Keywords: alternative splicing; blocked amino end; cell binding; coiled coil; extracel  
 F:1-25/Domin: signal sequence #status predicted <SIG>  
 F:26-3176/Product: collagen alpha 3(VI) chain #status predicted <MAT1>  
 F:26-2037/Domin: amino-terminal nonhelical #status predicted <ANH>  
 F:26-30,237-3176/Product: collagen alpha 3(VI) chain, splice form A9/N10(-) #status pred  
 F:37-203/Domin: von Willebrand factor type A repeat homology <W01>  
 F:240-405/Domin: von Willebrand factor type A repeat homology <W02>  
 F:443-608/Domin: von Willebrand factor type A repeat homology <W03>  
 F:637-602/Domin: von Willebrand factor type A repeat homology <W04>  
 F:835-999/Domin: von Willebrand factor type A repeat homology <W05>  
 F:1027-1191/Domin: von Willebrand factor type A repeat homology <W06>  
 F:1331-1394/Domin: von Willebrand factor type A repeat homology <W07>  
 F:1434-1599/Domin: von Willebrand factor type A repeat homology <W08>  
 F:1537-1802/Domin: von Willebrand factor type A repeat homology <W09>  
 F:1836-2005/Domin: von Willebrand factor type A repeat homology <W10>  
 F:2038-2373/Region: interrupted helical  
 F:2040-2042/Region: cell attachment (R-G-D) motif  
 F:2136-2138/Region: cell attachment (R-G-D) motif  
 F:2148-2150/Region: cell attachment (R-G-D) motif  
 F:2154-2156/Region: cell attachment (R-G-D) motif  
 F:2370-2372/Region: cell attachment (R-G-D) motif  
 F:2374-3176/Domin: carboxyl-terminal nonhelical #status predicted <CNH>  
 F:2400-2571/Domin: von Willebrand factor type A repeat homology <W11>  
 F:2617-2800/Domin: von Willebrand factor type A repeat homology <W12>

F:2865-2986/Region: alanine/lysine/proline/threonine/valine-rich repeats  
 F:2987-3072/Domin: fibronectin type III repeat homology <FN3>  
 F:3111-3161/Domin: animal Kunitz-type proteinase inhibitor homology <API>  
 F:326/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predicted  
 F:108,116,202,251,2079,2331,2558,2677,2681,3036/Binding site: carbohydrate (Asn) (covale  
 F:2087/Disulfide bonds: interchain #status predicted  
 F:2100,2206,2239,2316,2319/Modified site: 4-hydroxyproline (Pro) #status experimental  
 F:2103,2209,2212,2322,2337/Binding site: carboxylate (Lys) (covalent) #status experi  
 F:2103,2209,2212,2322,2337/Modified site: 5-hydroxylysine (Lys) #status experimental  
 F:3111-3161,3120-3144,3136-3157/Disulfide bonds: #status predicted

Query Match 13.58; Score 471.5; DB 2; Length 3176;  
 Best Local Similarity 30.98; Pred. No. 1.5e-22;  
 Matches 122; Conservative 86; Mismatches 148; Indels 39; Gaps 12;

293 DLSFLIGSTSGRRRIKOLLADVAOLDGPAGRLMGVQYGNPATPHLKTHTN 352  
 39 DIFFLVSSWTIGEHFOLVREFLVDVKSALAGENDFHFLALVQNGNPHTEFLNTYRT 98  
 353 SRDLKTAIEKITORGSLNVGRAISFVTKNPFSSKANGNR--GAPNVVVVVVDGWPYDKV 410  
 99 KQEVLSHISMVSYIGTNQNGKLEVIYMSHLTKRAGSRAGDVPQYIVVLDTGHSKDGL 158  
 411 EASRLARESGINIFFTTGAABNE-KQYVEBNPANKAVCTRTGFSYSH--VQSMFG- 466  
 159 ALPSAEIKSADVNVFALGVDADEGALKEIASBP--LNMFMFULENFTSLHDIQNLVSC 216  
 467 LKHTLOPLVRCVDDTDLACSKTCLNSADIGFPIIDSSSGTGNFRVLQFVNTLKEFE 526  
 217 VHSVSP--ERAGDTLELK-DITRQDSADILFIDGSNNNGSVNFAVILDFLVLEKLP 273  
 527 ISDTRIGAVQYTYEQRLFEGFDKYSKPDILNAIKRVGWSGG--TSTGAALNFALQ 584  
 274 IGQQRGVGVQSPDERMTFSLDTSTKQVGVKALGF-AGGELANIGLALDFVFN 332  
 585 LFKSKRPNK-----RKLMTITDGRSYDVDRIPAMAHLKGVTTVAIGVMAAOELEV 639  
 333 HFRAGSGRVEESGPVLVLISAGPSSDEIRYGVVALKQASVPSFGIGQAASRAELQHI 392  
 640 ATPARDHSFVDFPNLHQYVRIIQTCTEENS 674  
 393 ATD-----DNLVFTVP-----EPRS 407

RESULT 7  
 S31212  
 collagen alpha 1(XIV) chain precursor, short form - chicken  
 C:Species: Gallus gallus (chicken)  
 C>Date: 11-Mar-1998 #sequence\_rev1sion 17-Apr-1998 #ext\_change 15-Sep-2003  
 C:Accession: S31212  
 R:Melchli, C.; Trueb, U.; Kessler, B.; Winterhalter, K.H.; Trueb, B.  
 Eur. J. Biochem. 212, 483-490, 1993  
 A:Title: Complete primary structure of chicken collagen XIV.  
 A:Reference number: S31211; MUID:93185668; PMID:8444186  
 A:Accession: S31212  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1857 <WAB>  
 A:Cross-references: UNIPARC:UPI000017123C; EMBL:X70792; NID:G288874; PIDN:CAA50063.1; PIR:  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993  
 C:Genetics:  
 A:Gene: COL14A1  
 C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer;  
 F:1-28/Domin: signal sequence #status predicted <SIG>  
 F:29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>  
 F:29-110/Domin: fibronectin type III repeat homology <FN3A>  
 F:156-320/Domin: von Willebrand factor type A repeat homology <W01>  
 F:352-433/Domin: fibronectin type III repeat homology <FN3B>  
 F:442-525/Domin: fibronectin type III repeat homology <FN3C>  
 F:534-614/Domin: fibronectin type III repeat homology <FN3D>  
 F:623-707/Domin: fibronectin type III repeat homology <FN3E>  
 F:741-823/Domin: fibronectin type III repeat homology <FN3F>  
 F:832-914/Domin: fibronectin type III repeat homology <FN3G>



F;922-1009/Domain: fibronectin type III repeat homology <FN3H>  
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 9.5%; Score 331; DB 2; Length 1857;  
Best Local Similarity 24.8%; Pred. No. 1,66-13;

Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

```

Qy      174  IPGTTAQPVTLMQLAVTVAVAFPTLLPPSPSAASTSIPRPSQVGHRSQEMD----- 227
Db      713  IVGTTAIPPT-----VTTTTTATTPKPTIAVFRT-----GVKNLVIDDETTSS 757

Qy      228  ---LMSATATYSSQNR-----PRADPGIORDPGSAFQKPVGADVSLGLVPKEELS 276
Db      758  LRVVWDISDHNAQOFRTVTLTAKGDRAEBAIMVPGQNTLLLP-----LLPDEYK 809

Qy      277  TQSL-----EPVSLGDPNCKIDSLFIDGSTSIGKRRFRIOQLADVAQALDIPGAP 330
Db      810  VTTTPYADGEGVSAPGKTLPLS-----APRNLRVSDENWRRLISWD-APPSP 859

Qy      331  LMG--VVOYGDN---PATFHNKTHNSRDLKTAIEKITQRGLSLVNGRAISFVTKNFPS 385
Db      860  TWGRIYKISINVGPA---LETFVGD-DINTIL-----ILNLFSGTEYSVVFAS 906

Qy      386  KANG---NRSGAPNVVVVWDGWPDKVEASRLAR---ESGINIFITIEGAENKQY 439
Db      907  YSTGFSDALTGVAKTLVLTGVTNLDYQVMTSLCAQWQLRHATAVRVVIESLVGKKQ- 965

Qy      440  VVEPNFANKAVCTNGFYSL--HVQSWFGLHKTLO----- 472
Db      966  --EVNLGG-GVPR-HCFPELMPGTEYKISVHAQLOEIEGPVAVSIMETTLPPPTQPTSPS 1021

Qy      473  -----PLVKRVGCTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQPVNTLTKE 524
Db      1022  TTLPPPTIPPAKEVCAAK-----ADLVFLVDSWMSIGDDNFNKIISLYSTVGA 1071

Qy      525  FE-ISDTRIGAVQYTYEQRLEFGPKYSSKPDILNAIKRVGWSGCTGGAINFAL 583
Db      1072  LDKIGPDGTQVALIQSDDPRTFEKLNAYKTETTLLEAIQQLAYKGGNTKTGAIGHARE 1131

Qy      584  QLF-----KSKPKRKKMLILITDGRSYDDVRIPMAAHLKVITYAIGVMAAQEEL 637
Db      1132  VLFTEGAGMRKGIPI---KVLVITIDGRSODDVNKRVSREMQLDGFSPFALGVADADYSELV 1188

Qy      638  VIATHPARDHSFVDEFDNLHQVVRPIIIONIC 669
Db      1189  NIGSKPSERHVFVDDPDAFTKIEDELITFVC 1220

```

# RESULT 8

S78476 collagen alpha 1(XIV) chain precursor, long form - chicken

C/Species: Gallus gallus (chicken)

C/Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004

C/Accession: S78476; S31211

R/Trueb, B. submitted to the EMBL Data Library, January 1993

A/Accession number: S78476

A/Accession: S78476

A/Molecule type: mRNA

A/Residues: 1-1888 <TRU>

A/Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:Q288672; PII

R/Welchli, C.; Trueb, U.; Kessler, B.; Winterhalter, K.H.; Trueb, B.

Eur. J. Biochem. 212, 483-490, 1993

A/Title: Complete primary structure of chicken collagen XIV.

A/Reference number: S31211; MUID:93185668; PMID:8444186

A/Accession: S31211

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-416;11460-1811,1843-1888 <MAE>

A/Cross-references: UNIPARC:UPI00001773F4; UNIPARC:UPI00001773F5; EMBL:X70793

C/Genetics:

A/Gene: Coll14A1

C/Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trine

F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>

F;29-110/Domain: fibronectin type III repeat homology <FN3A>

F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>

F;352-433/Domain: fibronectin type III repeat homology <FN3B>

F;442-525/Domain: fibronectin type III repeat homology <FN3C>

F;534-614/Domain: fibronectin type III repeat homology <FN3D>

F;623-707/Domain: fibronectin type III repeat homology <FN3E>

F;741-823/Domain: fibronectin type III repeat homology <FN3F>

F;832-914/Domain: fibronectin type III repeat homology <FN3G>

F;922-1009/Domain: fibronectin type III repeat homology <FN3H>

F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 9.5%; Score 331; DB 2; Length 1888;  
Best Local Similarity 24.8%; Pred. No. 1,76-13;  
Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

```

Qy      174  IPGTTAQPVTLMQLAVTVAVAFPTLLPPSPSAASTSIPRPSQVGHRSQEMD----- 227
Db      713  IVGTTAIPPT-----VTTTTTATTPKPTIAVFRT-----GVKNLVIDDETTSS 757

Qy      228  ---LMSATATYSSQNR-----PRADPGIORDPGSAFQKPVGADVSLGLVPKEELS 276
Db      758  LRVVWDISDHNAQOFRTVTLTAKGDRAEBAIMVPGQNTLLLP-----LLPDEYK 809

Qy      277  TQSL-----EPVSLGDPNCKIDSLFIDGSTSIGKRRFRIOQLADVAQALDIPGAP 330
Db      810  VTTTPYADGEGVSAPGKTLPLS-----APRNLRVSDENWRRLISWD-APPSP 859

Qy      331  LMG--VVOYGDN---PATFHNKTHNSRDLKTAIEKITQRGLSLVNGRAISFVTKNFPS 385
Db      860  TWGRIYKISINVGPA---LETFVGD-DINTIL-----ILNLFSGTEYSVVFAS 906

Qy      386  KANG---NRSGAPNVVVVWDGWPDKVEASRLAR---ESGINIFITIEGAENKQY 439
Db      907  YSTGFSDALTGVAKTLVLTGVTNLDYQVMTSLCAQWQLRHATAVRVVIESLVGKKQ- 965

Qy      440  VVEPNFANKAVCTNGFYSL--HVQSWFGLHKTLO----- 472
Db      966  --EVNLGG-GVPR-HCFPELMPGTEYKISVHAQLOEIEGPVAVSIMETTLPPPTQPTSPS 1021

Qy      473  -----PLVKRVGCTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQPVNTLTKE 524
Db      1022  TTLPPPTIPPAKEVCAAK-----ADLVFLVDSWMSIGDDNFNKIISLYSTVGA 1071

Qy      525  FE-ISDTRIGAVQYTYEQRLEFGPKYSSKPDILNAIKRVGWSGCTGGAINFAL 583
Db      1072  LDKIGPDGTQVALIQSDDPRTFEKLNAYKTETTLLEAIQQLAYKGGNTKTGAIGHARE 1131

Qy      584  QLF-----KSKPKRKKMLILITDGRSYDDVRIPMAAHLKVITYAIGVMAAQEEL 637
Db      1132  VLFTEGAGMRKGIPI---KVLVITIDGRSODDVNKRVSREMQLDGFSPFALGVADADYSELV 1188

Qy      638  VIATHPARDHSFVDEFDNLHQVVRPIIIONIC 669
Db      1189  NIGSKPSERHVFVDDPDAFTKIEDELITFVC 1220

```

# RESULT 9

A54849

collagen alpha 1(VII) chain precursor - human

N/Alternate names: procollagen alpha 1(VII) chain

C/Species: Homo sapiens (man)

C/Date: 04-Nov-1994 #sequence\_revision 04-Nov-1994 #text\_change 09-Jul-2004

C/Accession: A54849; P00844; S16316; I56328; A30266; I84686

R/Christiano, A.M.; Greenspan, D.S.; Lee, S.; Utico, J.

J. Biol. Chem. 269, 20256-20262, 1994

A/Title: Cloning of human type VII collagen. Complete primary sequence of the alpha (VII)

A/Reference number: A54849; MUID:94327588; PMID:8051117

A/Accession: A54849

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-2944 <CHR>



A:Cross-references: UNIPROT:002388; UNIPARC:UPI000017A138; GB:L02870; NID:G987124; PIDN: R.Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.  
Biochem. Biophys. Res. Commun. 183, 958-963, 1992  
A:Title: Molecular cloning and characterization of type VII collagen cDNA.  
A:Reference number: P10844; MUID:92231902; PMID:1567409  
A:Accession: P10844  
A:Molecule type: mRNA  
A:Residues: 'EPR', 340-475, 'ALSTASHSTLCWRATRMHPCNRGSHWTRACPCNRPASHRARAG', 524-528, 'C',  
A:Cross-references: UNIPARC:UPI000017A139; DDBJ:D11152; DDBJ:D13694; NID:G453698; PIDN: E  
A:Experimental source: keratinocyte  
A:Note: the authors translated the codon ACC for residues 394 and 397 as Tyr  
R.Parente, M.G.; Chung, L.C.; Rymmenen, J.; Woodley, D.T.; Wynn, K.C.; Bajer, E.A.; Mac  
Proc. Natl. Acad. Sci. U.S.A. 86, 6931-6935, 1991  
A:Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.  
A:Reference number: S16316; MUID:91334380; PMID:1871109  
A:Accession: S16316  
A:Molecule type: mRNA  
A:Residues: 815-892, 'E', 894-1439 <PAR>  
A:Cross-references: UNIPARC:UPI000016A722; GB:M65158; GB:S49017; NID:G180914; PIDN:AAA96  
A:Experimental source: keratinocyte  
J.Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Priyaanah, P.S.; Cook, M.E.; Wright, J.;  
J. Invest. Dermatol. 99, 691-696, 1992  
A:Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot  
A:Reference number: 156328; MUID:93107742; PMID:1469284  
A:Accession: 156328  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 'EPR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>  
A:Cross-references: UNIPARC:UPI000016B3AC; GB:S51236; NID:G262308; PIDN:AA24637.1; PID:  
J. Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgess, R.E.  
J. Biol. Chem. 264, 3822-3828, 1989  
A:Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagenase  
A:Reference number: A30296; MUID:89139437; PMID:2537292  
A:Accession: A30296  
A:Molecule type: Protein  
A:Residues: 'AY', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E', 2032, 'C', 2034-2041, '  
A:Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;  
A:Note: two reported peptides cannot be reliably located  
R.Greenpan, D.S.  
Hum. Mol. Genet. 2, 273-278, 1993  
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous  
A:Reference number: 148103; MUID:93271985; PMID:8499916  
A:Accession: 148103  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 2395-2871, 'S', 2873-2944 <RE2>  
A:Cross-references: UNIPARC:UPI000016A724; GB:L06862; NID:G388713; PIDN:AAA89196.1; PID:  
R.Christiano, A.M.; Rymmenen, M.; Uitto, J.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994  
A:Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser sube  
A:Reference number: A55255; MUID:94224777; PMID:8170945  
A:Contents: annotation  
A:Comment: Prolines and lysines at the third position of the tripeptide repeating unit c  
ed and subsequently O-glycosylated.  
C:Genetics:  
A:Gene: GDB:COL7A1; EBR1; EBD1; EB  
A:Cross-references: GDB:128750; OMIM:120120  
A:Map position: 3p21.3-3p21.3  
A:Note: defects in this gene can result in dominant and recessive dystrophic epidermolys  
C:Note: there are 118 introns  
C:Complex: type VII collagen is probably a homotrimer  
C:Function:  
A:Description: structural component of extracellular polymer associated with anchoring f  
C:Keywords: coll; coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>  
F:17-1253/Domain: amino-terminal nonhelical #status predicted <NC1>  
F:36-201/Domain: von Willebrand factor type A repeat homology <WVA1>  
F:36-201/Domain: von Willebrand factor type A repeat homology <WVA1>  
F:231-318/Domain: fibronectin type III repeat homology <FN1>  
F:337-413/Domain: fibronectin type III repeat homology <FN2>  
F:414-502/Domain: fibronectin type III repeat homology <FN3>  
F:508-593/Domain: fibronectin type III repeat homology <FN4>  
F:598-683/Domain: fibronectin type III repeat homology <FN5>

F:686-771/Domain: fibronectin type III repeat homology <FN6>  
F:776-862/Domain: fibronectin type III repeat homology <FN7>  
F:864-992/Domain: fibronectin type III repeat homology <FN8>  
F:954-1045/Domain: fibronectin type III repeat homology <FN9>  
F:1052-1219/Domain: von Willebrand factor type A repeat homology <WVA2>  
F:1170-1172/Region: cell attachment (R-G-D) motif  
F:1189-1253/Region: cysteine/proline-rich  
F:1254-1253/Region: interrupted helical  
F:1334-1336/Region: cell attachment (R-G-D) motif  
F:2008-2010/Region: cell attachment (R-G-D) motif  
F:2553-2555/Region: cell attachment (R-G-D) motif  
F:2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>  
F:2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
F:337,786,1109/Binding site: carbohydrate (asn) (covalent) #status predicted  
F:2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status exper  
F:2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental  
F:2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental  
F:2654,2802,2804/Disulfide bonds: interchain #status predicted  
Query Match 9.4%; Score 329.5; DB 2; Length 2944;  
Best Local Similarity 35.7%; Pred. No. 4.1e-13;  
Matches 80; Conservative 37; Mismatches 86; Indels 19; Gaps 4;  
Qy 470 TLDPVLRVC-----DTRLACSKTCUNADIGFVIDGSSVGTGNFRVYLQ 516  
Db 2 TLRLVALACGILAEAPRVRAQHRRVCTCR--LYADIVFLDGGSSISGRNFRVRS 59  
Qy 517 FVNTNLTKEFE--ISDTRIGAOYTYEQLEGFQDKSKRPILNAIKVGVNCGSTST 574  
Db 60 FLEGVLVPSGAAASACQVRATVQYSDPRTFGLDLSGGGVATRAIRLSYKSGNTRT 119  
Qy 575 GAAMFALAEOLF--KSKPKMKRLMLITDGRSDVDVRIAPMAAHLGVTVAIGVMAA 632  
Db 120 GAALHVAHDVFLPQLARPEVPVVCILITDGSQODLVDTAAQNLKGGCVLPAFGIRKAD 179  
Qy 633 QEELEVIATTPADHSFFVDEPNLHOYVPRITONICTEFSNP 676  
Db 180 PEEKIRVASOPTSDFFEFVNDFFSILRLPLDVRVCTTAGVPV 223  
RESULT 10  
A45974  
collagen alpha 1(XIV) chain precursor, short form 2 - chicken  
N:Alternate names: undulin  
C:Species: Gallus gallus (chicken)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A45974; S30085; S22916; S17035; S20833  
R:Gene: GDB: A45974; S30085; S22916; S17035; S20833  
J. Biol. Chem. 268, 12177-12184, 1993  
A:Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' regions  
A:Reference number: A45974; MUID:93280195; PMID:8505337  
A:Accession: A45974  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-1747 <GER>  
A:Cross-references: UNIPROT:P32018; UNIPARC:UPI0000173C47  
A:Experimental source: embryo skin  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBI:133364, NCBI:P.133365)  
R:ApTe, S.S.  
submitted to the EMBL Data Library, March 1992  
A:Reference number: S30085  
A:Accession: S30085  
A:Molecule type: mRNA  
A:Residues: 1472-1660 <APT>  
A:Cross-references: UNIPARC:UPI00000006A2; EMBL:X65122; NID:G62871; PIDN:CAA46238.1; PID:  
R:Trueb, J.; Trueb, B.  
Eur. J. Biochem. 207, 549-557, 1992  
A:Title: Type XIV collagen is a variant of undulin.  
A:Reference number: S22916; MUID:92339443; PMID:1339349  
A:Accession: S22916  
A:Status: preliminary





A:Reference number: S23676; MUID:87260814; PMID:3496594  
 A:Accession: S23676  
 A:Molecule type: DNA  
 A:Residues: 2731-2813 <COL>  
 A:Cross-references: UNIPARC:UPI000014240A; EMBL:M16945  
 R:Bonthron, D.; Orr, E.C.; Mitscock, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.  
 Nucleic Acids Res. 14, 7125-7127, 1986  
 A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.  
 A:Reference number: A25298; MUID:87016349; PMID:3489923  
 A:Accession: A25298  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-2813 <BOX>  
 A:Cross-references: UNIPARC:UPI000017431B; EMBL:X04385  
 R:Verweij, C.L.; Diegaarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 1839-1847, 1986  
 A:Title: Full-length von Willebrand factor (VWF) cDNA encodes a highly repetitive protei  
 A:Reference number: A91044; MUID:87004550; PMID:3019665  
 A:Accession: A25469  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>  
 A:Cross-references: UNIPARC:UPI000017431C; EMBL:X04146  
 A:Note: this sequence has been revised in reference A91056  
 R:Verweij, C.L.; Diegaarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 3074, 1986  
 A:Reference number: A91056  
 A:Accession: A25366  
 A:Molecule type: mRNA  
 A:Residues: 1021-1030 <VE2>  
 A:Cross-references: UNIPARC:UPI000017431D  
 A:Note: this is a revision to the sequence from reference A91044  
 R:Shelton-Inioes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.  
 Biochem. Biophys. Res. Commun. 144, 657-665, 1987  
 A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated  
 A:Reference number: S23618; MUID:87213253; PMID:3495266  
 A:Accession: S23618  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <SH2>  
 A:Cross-references: UNIPARC:UPI000016830A; EMBL:M17588; NID:G799330; PIDN:AAA65940.1; PI  
 A:Accession: S23645  
 A:Molecule type: protein  
 A:Residues: 23-56 <SH3>  
 A:Cross-references: UNIPARC:UPI000017431E  
 R:Sadler, J.E.; Shelton-Inioes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985  
 A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand fact  
 A:Reference number: A94060; MUID:86016708; PMID:2864688  
 A:Accession: A94060  
 A:Molecule type: mRNA  
 A:Residues: 'WA', '739', 'C', '744-769', 'H', '771-788', 'A', '790-803', 'S', '805-873', '1289-1471', 'D', '1473-  
 A:Cross-references: UNIPARC:UPI000017431F; UNIPARC:UPI0000174320  
 A:Note: the authors translated the codon TCG for residue 2168 as Cys  
 R:Shelton-Inioes, B.B.; Titani, K.; Sadler, J.E.  
 Biochemistry 25, 3164-3171, 1986  
 A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated dc  
 A:Reference number: A90504; MUID:86265894; PMID:3488076  
 A:Accession: A90504  
 A:Molecule type: mRNA  
 A:Residues: 781-788, 'A', '790-1424 <SHE>  
 A:Cross-references: UNIPARC:UPI0000174321  
 A:Note: 852-Gln, 857-Asp, and 1381-Thr were also found  
 R:Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.; C  
 Science 228, 1401-1406, 1985  
 A:Title: Human von Willebrand factor (VWF): isolation of complementary DNA (cDNA) clones  
 A:Reference number: A44178; MUID:85244588; PMID:3874428  
 A:Accession: A44178  
 A:Molecule type: mRNA  
 A:Residues: 2621-2813 <GIN>  
 A:Cross-references: UNIPARC:UPI0000168307; EMBL:X03028; NID:G340308; PIDN:AAA61293.1; PI  
 R:Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; va  
 Nucleic Acids Res. 13, 4699-4717, 1985  
 A:Title: Construction of cDNA coding for human von Willebrand factor using antibody prob  
 A:Reference number: S07363; MUID:85265603; PMID:3875078  
 A:Accession: S07363

A:Molecule type: mRNA  
 A:Residues: 2731-2813 <VE3>  
 A:Cross-references: UNIPARC:UPI000014240A; EMBL:X02672; NID:G37939; PIDN:CAA26503.1; PID:  
 R:Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Lang, E.H.; Living  
 Cell 41, 49-56, 1985  
 A:Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a r  
 A:Reference number: S23678; MUID:85201687; PMID:3873280  
 A:Accession: S23678  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <LYN>  
 A:Cross-references: UNIPARC:UPI000014240A; EMBL:X03028  
 R:Titani, K.; Kumar, S.; Tekio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.;  
 Biochemistry 25, 3171-3184, 1986  
 A:Title: Amino acid sequences of human von Willebrand factor.  
 A:Reference number: A90505; MUID:86269895; PMID:3524673  
 A:Accession: A90505  
 A:Molecule type: protein  
 A:Residues: 764-788, 'A', '790-1471', 'D', '1473-2813 <TTT>  
 A:Cross-references: UNIPARC:UPI0000174322  
 A:Note: 789-Thr was also found  
 R:Chopek, M.W.; Girna, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.  
 Biochemistry 25, 3146-3155, 1986  
 A:Title: Human von Willebrand factor: a multivalent protein composed of identical subunit  
 A:Reference number: A23464; MUID:86269892; PMID:3015199  
 A:Accession: A23464  
 A:Molecule type: protein  
 A:Residues: 764-773; 2803-2813 <CHO>  
 A:Cross-references: UNIPARC:UPI0000174323; UNIPARC:UPI0000174324  
 R:Ident, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggieri, Z.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990  
 A:Title: Identification of a cleavage site directing the immunochemical detection of mole  
 A:Reference number: A36013; MUID:90349604; PMID:2385594  
 A:Accession: A36013  
 A:Molecule type: protein  
 A:Residues: 1606-1617 <DEN>  
 A:Cross-references: UNIPARC:UPI0000174325  
 R:Ray, P.O.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.M.;  
 Science 232, 995-998, 1986  
 A:Title: Propylpeptide of von Willebrand factor circulates in blood and is identical to  
 A:Reference number: A60913; MUID:86208144; PMID:3486471  
 A:Accession: A60913  
 A:Molecule type: protein  
 A:Residues: 576-590 <FAR>  
 A:Cross-references: UNIPARC:UPI0000174326  
 C:Genetics:  
 A:Gene: GDB:VWF  
 A:Cross-references: GDB:119125; OMIM:193400  
 A:Map position: 12p13.3-12p13.2  
 A:Intons: 19/1, 74/1, 108/2, 178/1, 218/3, 292/1, 333/1, 370/2, 386/1, 431/3, 478/1, 511  
 5/1, 1724/1, 1771/1, 1819/1, 1874/1, 1888/3, 1948/1, 2021/3, 2086/1, 2200/1, 2266/3, 2303  
 C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von v  
 C:Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:32-763/Product: von Willebrand antigen II #status predicted <MA1>  
 F:34-386/Domain: type D repeat 1 <DD1>  
 F:387-745/Domain: type D repeat 2 <DD2>  
 F:698-700/Region: cell attachment (R-G-D) motif  
 F:764-2813/Product: von Willebrand factor #status predicted <MA2>  
 F:784-865/Domain: D' <DDD>  
 F:788-833, 2216-2261/Region: duplication  
 F:826-853, 2400-2515, 2544-2662/Region: duplication  
 F:842-1130, 1934-2203/Region: duplication  
 F:866-1241/Domain: type D repeat 3 <DD3>  
 F:1275-1443/Domain: von Willebrand factor type A repeat homology <VMA1>  
 F:1496-1654/Domain: von Willebrand factor type A repeat homology <VMA2>  
 F:1689-1854/Domain: von Willebrand factor type A repeat homology <VMA3>  
 F:1947-2295/Domain: type D repeat 4 <DD4>  
 F:2296-2330/Domain: type B repeat 1 <VB1>  
 F:2340-2365/Domain: type B repeat 2 <VB2>  
 F:2375-2399/Domain: type B repeat 3 <VB3>  
 F:2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>  
 F:2507-2509/Region: cell attachment (R-G-D) motif  
 F:2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>



**THIS PAGE BLANK (USPTO)**

OM protein - protein search, using sw model  
Run on: September 5, 2006, 20:01:58 ; Search time 199 Seconds  
(without alignments)

Title: US-10-063-538-34  
Perfect score: 3502  
Sequence: 1 MRYVYLTMKSVIEMFLVL.....QYVPRITQICTEFNQPRN 678  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
2589679 sege, 457216429 residues  
Total number of hits satisfying chosen parameters: 2589679  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :

A\_Geneseq 8: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6674	standard;	protein;	678	AA.	
DE	Membrane-bound protein	PRO1277.				
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 3;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 2						
ID	AAU29098	standard;	protein;	678	AA.	
DE	Human PRO polypeptide sequence #75.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 4;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 3						
ID	AAB87542	standard;	protein;	678	AA.	
DE	Human PRO1277.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 4;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 4						
ID	AAB65197	standard;	protein;	678	AA.	
DE	Human PRO1277 (UNQ647) protein sequence SEQ ID NO:179.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 4;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 5						
ID	ABG95867	standard;	protein;	678	AA.	
DE	Human secreted/transmembrane protein PRO1277.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 5;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 6						
ID	ABU58474	standard;	protein;	678	AA.	
DE	Human PRO polypeptide #75.					

PN	US2003027272-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 7						
ID	ABU88022	standard;	protein;	678	AA.	
DE	Novel human secreted and transmembrane protein PRO1277.					
PN	US2003032127-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 8						
ID	ABU84337	standard;	protein;	678	AA.	
DE	Human secreted/transmembrane protein (PRO) #75.					
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 9						
ID	ABR66211	standard;	protein;	678	AA.	
DE	Human secreted polypeptide PRO1277, SEQ ID NO:150.					
PN	US2003027278-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 10						
ID	ABR65601	standard;	protein;	678	AA.	
DE	Human secreted polypeptide PRO1277, SEQ ID NO:150.					
PN	US2003036159-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 11						
ID	ABU99541	standard;	protein;	678	AA.	
DE	Human secreted/transmembrane protein (PRO) #75.					
PN	US2003040070-A1.					
PD	27-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 12						
ID	ABU58012	standard;	protein;	678	AA.	
DE	Human PRO polypeptide #44.					
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 13						
ID	ABU59090	standard;	protein;	678	AA.	
DE	Novel human secreted or transmembrane protein PRO1277.					
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 14						
ID	ABU82602	standard;	protein;	678	AA.	
DE	Human secreted/transmembrane protein PRO1277.					
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 15						
ID	ABU82780	standard;	protein;	678	AA.	
DE	Human PRO polypeptide #75.					
PN	US2003032113-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3502;	DB 6;	Length 678;		
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;				
RESULT 16						
ID	ABU89901	standard;	protein;	678	AA.	
DE	Novel human secreted and transmembrane protein PRO1277.					
PN	US2003036147-A1.					
PD	20-FEB-2003.					

Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 17  
ID ABR68150 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 18  
ID ABU60521 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein, #69.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 19  
ID ABU96203 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 20  
ID ABU92634 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 21  
ID ABU08711 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 22  
ID ABO02763 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 23  
ID ABR74917 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 24  
ID ABR94679 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 25  
ID ABU13903 standard; protein; 678 AA.  
DE Human PRO1277 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 26  
ID ABU85652 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 27  
ID ABU98812 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 28  
ID ABU98027 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 29  
ID ABU91733 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 30  
ID ABU89426 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 31  
ID ABU86267 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 32  
ID ABU67480 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 33  
ID ABU80508 standard; protein; 678 AA.  
DE Human PRO protein #75.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 34  
ID ABU72488 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 35  
ID ABU90892 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 36  
ID ABO33951 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.



PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 37  
ID ABR9426 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 38  
ID ABR9816 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 39  
ID ABO1639 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 40  
ID ABR92239 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 41  
ID ABO18880 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 42  
ID ABR78301 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 43  
ID ABR71968 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 44  
ID ABU85037 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 45  
ID ABO00176 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 46  
ID ABO11508 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.

PN US2003036124-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 47  
ID ABO02153 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 48  
ID ABO8727 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 49  
ID ABO83422 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 50  
ID ABO06223 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 51  
ID ABR59259 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 52  
ID ABO09321 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 53  
ID ABO19185 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 54  
ID ABO11203 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 55  
ID ABR66821 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 56  
ID ABO16034 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003040060-A1.  
PD 27-FEB-2003.

Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 57  
ID ABO13740 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 58  
ID ABU71522 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 59  
ID ABU65643 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein, SEQ ID 150.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 60  
ID ABO07491 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 61  
ID ABO03678 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 62  
ID ABR67126 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 63  
ID ABO15729 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 64  
ID ABU56010 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein, PRO1277.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 65  
ID ABU72303 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 66  
ID ABU6538 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032102-A1.  
PD 13-FEB-2003.

Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 67  
ID ABU95283 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 68  
ID ABU71186 standard; protein; 678 AA.  
DE Human PRO1277 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 69  
ID ABO07796 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 70  
ID ABR70037 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 71  
ID ABR69370 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 72  
ID ABO01511 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 73  
ID ABU81313 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 74  
ID ABR60110 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 75  
ID ABU90976 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 76  
ID ABR67845 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027269-A1.  
PD 06-FEB-2003.

Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 77  
ID ABR65233 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 78  
ID ABR68455 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 79  
ID ABR71867 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN 13-FEB-2003.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 80  
ID AB059237 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein, #69.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 81  
ID AB05347 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 82  
ID AB089037 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 83  
ID AB083117 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 84  
ID AB094973 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 85  
ID AB090521 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 86  
ID AB084032 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 87  
ID AB093683 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 88  
ID AB025934 standard; protein; 678 AA.  
DE Human PRO1277 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 89  
ID ABR64928 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 90  
ID AB027297 standard; protein; 678 AA.  
DE Human secreted/transmembrane polypeptide PRO1277.  
PN US200309012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 91  
ID ABR68760 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 92  
ID AB006576 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 93  
ID ABR99121 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 94  
ID AB057005 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 95  
ID AB085957 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003023300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 96  
ID AB082244 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 97  
ID ABU87255 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 98  
ID ABU83727 standard; protein; 678 AA.  
DE Human secreted/cranmembrane protein (PRO) #75.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 99  
ID ABO08101 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 100  
ID ABU92492 standard; protein; 678 AA.  
DE Human secreted/cranmembrane protein PRO1277.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 101  
ID ABU81812 standard; protein; 678 AA.  
DE Novel human secreted and cranmembrane protein PRO1277.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 102  
ID ABU65976 standard; protein; 678 AA.  
DE Novel human secreted and cranmembrane protein PRO1277.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 103  
ID ABU81162 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 104  
ID ABU59805 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 105  
ID ABU93993 standard; protein; 678 AA.  
DE Novel human secreted and cranmembrane protein PRO1277.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 106  
ID ABU99846 standard; protein; 678 AA.  
DE Novel human secreted and cranmembrane protein PRO1277.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 107

ID ABR66516 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 108  
ID ABR90934 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 109  
ID ABO53277 standard; protein; 678 AA.  
DE Novel human secreted and cranmembrane protein PRO1277.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 110  
ID ABU58943 standard; protein; 678 AA.  
DE Human secreted/cranmembrane protein, #69.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 111  
ID ABU94361 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 112  
ID ABU79243 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 113  
ID ABU86572 standard; protein; 678 AA.  
DE Human secreted/cranmembrane protein (PRO) #75.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 114  
ID ABU86877 standard; protein; 678 AA.  
DE Novel human secreted and cranmembrane protein PRO1277.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 115  
ID ABU94666 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 116  
ID ABO04593 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 117

ID ABR70342 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 118  
ID ABR92321 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 119  
ID ABR98507 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 120  
ID ABR65906 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 121  
ID ABR64623 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 122  
ID ABR59386 standard; protein; 678 AA.  
DE Novel human secreted or transmembrane protein PRO1135.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 123  
ID ABR79548 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 124  
ID ABR92939 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 125  
ID ABR95898 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 126  
ID ABR91118 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 127  
ID ABR90211 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.

PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 128  
ID ABR09626 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 129  
ID ABR10898 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 130  
ID ABR70952 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 131  
ID ABR98279 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 132  
ID ABR87560 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 133  
ID ABR91428 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 134  
ID ABR89284 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003036334-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 135  
ID ABR84642 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 136  
ID ABR69732 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 137  
ID ABR80109 standard; protein; 678 AA.  
DE Human PRO protein #75.  
PN US2003036139-A1.

PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 138  
ID ABU82491 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 139  
ID ABU92152 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 140  
ID ABU93378 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 141  
ID ABO09931 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 142  
ID ABO09016 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 143  
ID ABU96455 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 144  
ID ABU10658 standard; protein; 678 AA.  
DE Human PRO polypeptide #44.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 145  
ID ABU10584 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein #75.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 146  
ID ABU81610 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 147  
ID ABU72125 standard; protein; 678 AA.

DE Human PRO polypeptide #17.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 148  
ID ABU95593 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 149  
ID ABU96802 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 150  
ID ABR70647 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 151  
ID ABO04998 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 152  
ID ABO08406 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 153  
ID ABU88549 standard; protein; 678 AA.  
DE Human secreted and transmembrane polypeptide PRO1277.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 154  
ID ABO34063 standard; protein; 678 AA.  
DE Human PRO1277 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 155  
ID ABO05613 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 156  
ID ABR74002 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 157

ID ABR95594 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 158  
ID ABR80891 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 159  
ID ABR81196 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 160  
ID ABR00892 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 161  
ID ABR88494 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 162  
ID ABR77315 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 163  
ID ABR028799 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 164  
ID ABO31544 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 165  
ID ABR07961 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 166  
ID ABO40441 standard; protein; 678 AA.

DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 167  
ID ABO35866 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 168  
ID ABO44005 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 169  
ID ADA77902 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 170  
ID ABR24800 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 171  
ID ABO03068 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 172  
ID ABR90324 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 173  
ID ABR17238 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 174  
ID ABR94984 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 175  
ID ABR95289 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 176  
ID ADB17091 standard; protein; 678 AA.  
DE Human transmembrane PRO polypeptide (Segid 34).  
PD US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 177  
ID ABO21527 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PD US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 178  
ID ABR97791 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 179  
ID ABR87579 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 180  
ID AAM77620 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 181  
ID AAM27850 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 182  
ID AAM06131 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 183  
ID AAM03637 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 184  
ID AAM3508 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 185

ID AAM26325 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 186  
ID ABO48107 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PD US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 187  
ID ABR92849 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 188  
ID ABO24610 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 189  
ID ADA37690 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PD US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 190  
ID AAM11621 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 191  
ID AAM02722 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 192  
ID AAM16018 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PD US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 193  
ID ABO27579 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PD US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 194  
ID AAM29070 standard; protein; 678 AA.



DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 195  
ID ABO07046 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 196  
ID ABO21140 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 197  
ID ABO09486 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 198  
ID ABO41356 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 199  
ID ABO36171 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 200  
ID ABO43700 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 201  
ID ABO76400 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 202  
ID ABO76096 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 203  
ID ABO25715 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104542-A1.

PD 05-JUN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 204  
ID ABO26020 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 205  
ID ADA21376 standard; protein; 678 AA.  
DE Human secreted/transmembrane polypeptide PRO1277.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 206  
ID ABO03373 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 207  
ID ABO02458 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 208  
ID ABO44255 standard; protein; 678 AA.  
DE Human secreted/transmembrane polypeptide PRO 1277.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 209  
ID ABR90629 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 210  
ID ABR73697 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 211  
ID ABO16949 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 212  
ID ABR94374 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 213  
ID ABR75681 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003044929-A1.

PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 214  
ID ABR71257 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 215  
ID ABR93154 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 216  
ID ABR93459 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 217  
ID AD10163 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein, PRO1277.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 218  
ID ABR87884 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 219  
ID ABO27884 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 220  
ID ABO30019 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 221  
ID ABO33328 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 222  
ID ABO04916 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 223  
ID ABO08876 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 224  
ID ABO36476 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 225  
ID ABO35561 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 226  
ID ABO39526 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 227  
ID ABO10401 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 228  
ID ABO11926 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 229  
ID ABO52072 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 230  
ID ABO52377 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
RESULT 231  
ID AD119696 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;

RESULT 232  
ID ABO23695 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 233  
ID AD817279 standard; protein; 678 AA.  
DE Human transmembrane PRO polypeptide (Segid 34).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 234  
ID AD417707 standard; protein; 678 AA.  
DE Human PRO1277 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 235  
ID ABR97181 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 236  
ID ABR6969 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 237  
ID ABM11011 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 238  
ID ABM28155 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 239  
ID ABO32154 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 240  
ID ABM15281 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 241  
ID ABO06436 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.

PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 242  
ID ABM04247 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 243  
ID ABM22360 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 244  
ID ABM07656 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 245  
ID ABO40746 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 246  
ID ABM35393 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 247  
ID ABM33156 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 248  
ID ABO52682 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 249  
ID ABO50242 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 6; Length 678;  
Pred. No. 1.1e-306;  
RESULT 250  
ID ABU99236 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003040055-A1.  
PD 27-FEB-2003.

Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 251  
ID ABO04288 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 252  
ID ABO05918 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 253  
ID ABO18458 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 254  
ID ADA27815 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 255  
ID ABR97486 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 256  
ID ABR80586 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 257  
ID ABR01197 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 258  
ID ABR88799 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 259  
ID ABR13451 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 260  
ID ABR20835 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.

PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 261  
ID ABO41966 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 262  
ID ABO42576 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003048751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 263  
ID ABR10096 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 264  
ID ABO38611 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 265  
ID ABR32851 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 266  
ID ABR2265 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 267  
ID ABR74876 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 268  
ID ABR79694 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 269  
ID ABR96266 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 270  
ID ABO2417 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US200305986-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 271  
ID ABR86359 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 272  
ID ABR86664 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 273  
ID ABR16628 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 274  
ID ABR29680 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 275  
ID ABO29104 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 276  
ID ABR23885 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 277  
ID ABR23275 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 278  
ID ABR22055 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 279  
ID ABO22137 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

ID ABO37696 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 280  
ID ABR28460 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 281  
ID ABR28765 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 282  
ID ABR66409 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 283  
ID ABR75791 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 284  
ID ABR34071 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 285  
ID ABR34376 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 286  
ID ABO20307 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 287  
ID ABO21222 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 288  
ID ABO22137 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 289  
ID ADA20068 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US200305522-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 290  
ID ABO34183 standard; protein; 678 AA.  
DE Human secreted/transmembrane polypeptide PRO 1277.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 291  
ID ABR96571 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 292  
ID ADA94395 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 293  
ID ABR85749 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 294  
ID ABR9731 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 295  
ID ABR00587 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 296  
ID ABR00282 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 297  
ID ABO29714 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 298  
ID ABR23580 standard; protein; 678 AA.

DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 299  
ID ABR29375 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 300  
ID ABO38306 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 301  
ID ABO45606 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 302  
ID ABR20530 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 303  
ID ADA81421 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 304  
ID ABO16644 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 305  
ID ABO18270 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 306  
ID ABO22697 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 307  
ID ABO23002 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 308  
ID ABR92544 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 309  
ID ABR81501 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 310  
ID ABW77925 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 311  
ID ABR89714 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 312  
ID ABW26630 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 313  
ID ABW13756 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 314  
ID ABO28494 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 315  
ID ABO30324 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 316  
ID ABW07351 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 317

ID ABO03942 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 318  
ID ABO37086 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 319  
ID ABO41661 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 320  
ID ABO35256 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 321  
ID ABO25105 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 322  
ID ABO47497 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 323  
ID ABO47802 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 324  
ID ABO48412 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 325  
ID ABO51462 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 326  
ID ABO51767 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.

PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 327  
ID ABO50547 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 328  
ID ABR79671 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 329  
ID ABM16933 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 330  
ID ABO17965 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 331  
ID ABO20917 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 332  
ID ABR96876 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 333  
ID ADA38620 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003058780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 334  
ID ABM12231 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 335  
ID ABM16323 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 336  
ID ABM24190 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 337  
ID ABM14671 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 338  
ID ABM04552 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 339  
ID ABM06741 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 340  
ID ABM09181 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 341  
ID ABO39221 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 342  
ID ABM75486 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 343  
ID ABM25410 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 344  
ID ABM19920 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 345  
ID ABO46826 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049762-A1.



PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 346  
ID ABO47131 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 347  
ID ADA83219 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 348  
ID ABR71562 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 349  
ID ABR72172 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 350  
ID ABR98511 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 351  
ID ABO06881 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 352  
ID ABR84634 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 353  
ID ABR73392 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 354  
ID ABR76486 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 355  
ID ABR73087 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.

PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 356  
ID ABR18153 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 357  
ID ABO20612 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 358  
ID ABO25355 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 359  
ID ABO25660 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 360  
ID ABR94069 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 361  
ID ADA92741 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 362  
ID ABR79976 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 363  
ID ABR11316 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 364  
ID ABO32923 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 365  
ID ABO30629 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 366  
ID ABO30934 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 367  
ID ABM27240 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 368  
ID ABM29985 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 369  
ID ABM05521 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 370  
ID ABM15586 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 371  
ID ABM08571 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 372  
ID ABO42271 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003048748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 373  
ID ABO38001 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 374

ID ABO45911 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 375  
ID ABM66714 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 376  
ID ADB20262 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 377  
ID ABM19615 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 378  
ID ABO49327 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 379  
ID ABO49632 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 380  
ID ADA78514 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 381  
ID ABR88189 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 382  
ID ADA00365 standard; protein; 678 AA.  
DE Human secreted/transmembrane polypeptide PRO 1277.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 383  
ID ABM26935 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.

PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 384  
ID ABM03332 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 385  
ID ABO39831 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 6; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 386  
ID ABO49937 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 387  
ID ABO50852 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 388  
ID ABO5308 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 389  
ID ABR74612 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 390  
ID ABR77091 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 391  
ID ABM17848 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 392  
ID ABR35899 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 393

ID ABO21832 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 394  
ID ABO20002 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 395  
ID ABO24305 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 396  
ID ABR86054 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 397  
ID ABM10706 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 398  
ID ABR76705 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 399  
ID ABR89409 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 400  
ID ABM12536 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 401  
ID ABM05826 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 402  
ID ABO34951 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068728-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 403  
ID ABM03027 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 404  
ID ABM19005 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 405  
ID ABM19310 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 406  
ID ABO46521 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 407  
ID ABO49022 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 408  
ID ABR69065 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 409  
ID ABR89104 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 410  
ID ABR72477 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 411  
ID ABR74307 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 412  
ID ABO18575 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 413  
ID ABR80281 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 414  
ID ABM01502 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 415  
ID ABM02112 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 416  
ID ABR87274 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 417  
ID ABM12841 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 418  
ID ABM30595 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 419  
ID ADM24495 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 420  
ID ABO29409 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 421  
ID ABO31239 standard; protein; 678 AA.

DE Human secreted/transmembrane protein (PRO) #75.  
FN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 422  
ID ABM14366 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 423  
ID ABM09791 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 424  
ID ABO38916 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
FN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 425  
ID ABM34681 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 426  
ID ABO51157 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
FN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 427  
ID ABO03983 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
FN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 428  
ID ABO10453 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
FN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 429  
ID ABO53149 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
FN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 430  
ID ABR77696 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 431  
ID ABR78906 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 432  
ID ABO24000 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
FN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 433  
ID ABR93764 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 434  
ID ABO1807 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 435  
ID ABW78230 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003048764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 436  
ID ABR90019 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 437  
ID ADA22302 standard; protein; 678 AA.  
DE Human secreted/transmembrane polypeptide PRO1277.  
FN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 438  
ID ABM27545 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 439  
ID ABM13146 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
FN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 440  
ID ABO31849 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.

PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 441  
ID AEM14061 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 442  
ID AEM08266 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 443  
ID ABO40136 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 444  
ID ABM74571 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 445  
ID ABM33766 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 446  
ID AEM20225 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 447  
ID ABO48717 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 448  
ID ABO22519 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 449  
ID ABR72782 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 450  
ID ABO15424 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 451  
ID ABR85139 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 452  
ID ABO15119 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 453  
ID ABO17254 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 454  
ID ABM17543 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 455  
ID ADA06468 standard; protein; 678 AA.  
DE Human secreted/transmembrane PRO polypeptide #44.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 456  
ID ADA39161 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 457  
ID ABR85444 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 458  
ID ABM77010 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 459  
ID ABO28189 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 460  
ID ABM22970 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 461  
ID ABM30290 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 462  
ID ABM21750 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 463  
ID ABM21445 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 464  
ID ABM14976 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 465  
ID ABM41051 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 466  
ID ABM36781 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 467  
ID ABM37391 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 468  
ID ABM75181 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 469  
ID ABM33461 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 470  
ID ABM46216 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 471  
ID ADAB82585 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 472  
ID ADAB96187 standard; protein; 678 AA.  
DE Human PRO polypeptide #44.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 473  
ID ABM31815 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 474  
ID ABM31205 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 475  
ID ADAB83693 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein (PRO) #75.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 476  
ID ABM32120 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 477  
ID ABM32425 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 478  
ID ADAB68286 standard; protein; 678 AA.  
DE Human PRO1277 protein.

PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 479  
ID ADB68093 standard; protein; 678 AA.  
DE Human PRO1277 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 480  
ID AAM31510 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 481  
ID AAM30900 standard; protein; 678 AA.  
DE Human secreted polypeptide PRO1277, SEQ ID NO:150.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 482  
ID ADB90910 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 483  
ID ADC57659 standard; protein; 678 AA.  
DE Human PRO polypeptide #44.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 484  
ID ADC55023 standard; protein; 678 AA.  
DE Human PRO polypeptide #44.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 485  
ID ADC11890 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 486  
ID ADC06990 standard; protein; 678 AA.  
DE Human PRO1277 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 487  
ID ADC56312 standard; protein; 678 AA.  
DE Human PRO polypeptide #44.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
PD 100.0%; Pred. No. 1.1e-306;

RESULT 488  
ID ADC17169 standard; protein; 678 AA.  
DE Mammalian PRO polypeptide (SeqID 34).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 489  
ID ADC07367 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 490  
ID ADC11357 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 491  
ID ADC14667 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 492  
ID ADC52362 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 493  
ID ADC14479 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 494  
ID ADD08011 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 495  
ID ADC81836 standard; protein; 678 AA.  
DE Human PRO polypeptide #44.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 496  
ID ADD07478 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
RESULT 497  
ID ADC82369 standard; protein; 678 AA.  
DE Human PRO polypeptide #44.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3502; DB 7; Length 678;  
PD 100.0%; Pred. No. 1.1e-306;



```
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 498
ID ADD05623 standard; protein; 678 AA.
DE Human secreted/transmembrane.protein (PRO) #75.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 499
ID ADD08549 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 500
ID ADD06798 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 501
ID ADC83045 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 502
ID ADD55152 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 503
ID ADD36038 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 504
ID ADD56110 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 505
ID ADD54548 standard; protein; 678 AA.
DE Human PRO polypeptide #44.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 506
ID ADE26702 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 507
ID ADE26169 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003087305-A1.
PD 08-MAY-2003.

Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 508
ID ADE67106 standard; protein; 678 AA.
DE Human PRO1277 amino acid sequence SEQ ID NO:179.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 509
ID ADG01039 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 510
ID ADG08592 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 511
ID ADG02618 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 512
ID ADG01325 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 513
ID ADF95500 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 514
ID ADF95313 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 515
ID ADG12315 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 516
ID ADH24066 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
```

RESULT 517  
ID ADH34092 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 518  
ID ADH29925 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 519  
ID ADH23896 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 520  
ID ADH08975 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 521  
ID ADG85300 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 522  
ID ADH24576 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 523  
ID ADH37432 standard; protein; 678 AA.  
DE Human secreted and transmembrane protein PRO1277.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 524  
ID ADH02021 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 525  
ID ADH37602 standard; protein; 678 AA.  
DE Human secreted and transmembrane protein PRO1277.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 526  
ID ADH53511 standard; protein; 678 AA.

ID ADG85640 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 527  
ID ADH24236 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 528  
ID ADH38530 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 529  
ID ADG83651 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 530  
ID ADH29459 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 531  
ID ADH27575 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 532  
ID ADH37772 standard; protein; 678 AA.  
DE Human secreted and transmembrane protein PRO1277.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 533  
ID ADH37949 standard; protein; 678 AA.  
DE Human secreted and transmembrane protein PRO1277.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 534  
ID ADH57369 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 535  
ID ADH53511 standard; protein; 678 AA.

DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181636-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 536  
ID ADH93681 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 537  
ID ADH82017 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 538  
ID ADH49872 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 539  
ID ADI25382 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 540  
ID ADH90175 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 541  
ID ADI25552 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 542  
ID ADH97726 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 543  
ID ADI35360 standard; protein; 678 AA.  
DE Human PRO polypeptide #44.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 544  
ID ADI03574 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181656-A1.  
PA (GETH ) GENENTECH INC.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 545  
ID ADI11931 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 546  
ID ADH90005 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 547  
ID ADH99852 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 548  
ID ADH98406 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 549  
ID ADI11081 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 550  
ID ADI11591 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 551  
ID ADH98236 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 552  
ID ADH98576 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 553  
ID ADH98066 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 554  
ID AD105054 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 555  
ID AD103404 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 556  
ID AD104799 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 557  
ID ADH78253 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 558  
ID AD119597 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 559  
ID ADH90345 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 560  
ID AD103064 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 561  
ID ADH77913 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 562  
ID ADH97696 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 563  
ID AD101281 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 564  
ID AD101976 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 565  
ID AD103234 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 566  
ID AD111421 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 567  
ID AD102323 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 568  
ID AD111761 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 569  
ID AD105398 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 570  
ID ADH79470 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 571  
ID AD111427 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;

RESULT 572  
ID ADI05228 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 573  
ID ADH79640 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 574  
ID ADI01466 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 575  
ID ADI01636 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 576  
ID ADI01606 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 577  
ID ADH79610 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 578  
ID ADI04628 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 579  
ID ADI02764 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 580  
ID ADH78083 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 581

ID ADI25722 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 582  
ID ADI25892 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 583  
ID ADK65404 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 584  
ID ADH98746 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 585  
ID ADH79987 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 586  
ID ADL32756 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US200307396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 587  
ID ADM30290 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 588  
ID ADL93718 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 7; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 589  
ID ADC52172 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 590  
ID ADE74287 standard; protein; 678 AA.

Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 600		
ID ADH27745 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180912-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 601		
ID ADH25086 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180913-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 602		
ID ADH33718 standard; protein; 678 AA.		
DE Human PRO polypeptide #17.		
PN US2003181645-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 603		
ID ADG82799 standard; protein; 678 AA.		
DE Human PRO polypeptide #75.		
PN US2003215910-A1.		
PD 20-NOV-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 604		
ID ADH02361 standard; protein; 678 AA.		
DE Human PRO polypeptide #17.		
PN US2003180839-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 605		
ID ADH07968 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180845-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 606		
ID ADG69365 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180846-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 607		
ID ADH39186 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003180917-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 608		
ID ADH26080 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003068770-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;
RESULT 609		
ID ADH26080 standard; protein; 678 AA.		
DE Novel human secreted and transmembrane protein PRO1277.		
PN US2003068770-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3502; DB 8; Length 678;
Best Local Similarity	100.0%;	Pred. No. 1.1e-306;

RESULT 609  
ID ADG83926 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 610  
ID ADH19425 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US200328656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 611  
ID ADG85470 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 612  
ID ADH06264 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 613  
ID ADH30094 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 614  
ID ADH24406 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 615  
ID ADH33049 standard; protein; 678 AA.  
DE Human PRO polypeptide #75.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 616  
ID ADG69535 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 617  
ID ADH07798 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 618

ID ADG85810 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 619  
ID ADH39356 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180816-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 620  
ID ADH33548 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 621  
ID ADH33888 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 622  
ID ADH01098 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 623  
ID ADG69705 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 624  
ID ADH20918 standard; protein; 678 AA.  
DE Human secreted/transmembrane protein PRO1277.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 625  
ID ADH02191 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 626  
ID ADG69195 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 627  
ID ADG8580 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.

PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 628  
ID ADH24916 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 629  
ID ADH39533 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 630  
ID ADH19958 standard; protein; 678 AA.  
DE Human secreted/cransmembrane protein PRO1277.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 631  
ID ADH02531 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 632  
ID ADG69025 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 633  
ID ADH07628 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 634  
ID ADH86150 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 635  
ID ADH24746 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 636  
ID ADH25794 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180911-A1.

---

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 637  
ID ADH38360 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 638  
ID ADH57199 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 639  
ID ADH52187 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 640  
ID ADH49553 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 641  
ID ADH90515 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 642  
ID ADH11251 standard; protein; 678 AA.  
DE Human PRO polypeptide #17.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 643  
ID ADH98916 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 644  
ID ADH02146 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 645  
ID ADH90685 standard; protein; 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003183701-A1.  
PD 25-SEP-2003.



```
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 646
ID ADJ54788 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 647
ID ADJ98560 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 648
ID ADJ98730 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 649
ID ADJ78889 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187103-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 650
ID ADJ99123 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 651
ID ADJ99293 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 652
ID ADJ98911 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 653
ID ADJ79059 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 654
ID ADK00919 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 655
ID ADK14440 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 656
ID ADJ64559 standard; protein; 678 AA.
DE Human PRO polypeptide #75.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 657
ID ADM31455 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 658
ID ADM36502 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 659
ID ADM40307 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 660
ID ADM80889 standard; protein; 678 AA.
DE Human PRO polypeptide #17.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 661
ID ADM37915 standard; protein; 678 AA.
DE Novel human secreted and transmembrane protein PRO1277.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3502; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.1e-306;
RESULT 662
ID ADJ77729 standard; protein; 678 AA.
DE Neoplastic disease detection protein PRO1277.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) BATON D L.
PA (FLIV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3502; DB 9; Length 678;
```

Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 663  
ID AEA38448 standard; protein: 678 AA.  
DE Human secreted/transmembrane protein, #112.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 9; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 664  
ID AED50145 standard; protein: 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2005163766-A1.  
PD 28-JUL-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 9; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 665  
ID AEF12560 standard; protein: 678 AA.  
DE Human PRO1277 protein SEQ ID NO:34.  
PN US200608901-A1.  
PD 12-JAN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3502; DB 10; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 666  
ID AEF74249 standard; protein: 678 AA.  
DE Human PRO1277 protein SEQ ID NO:34.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATON ) EATON D L.  
PA (FILV ) FILVAROFF E.  
PA (GERR ) GERRITSEN M E.  
PA (GODO ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GRIM ) GRIMALDI J C.  
PA (GURN ) GURNEY A L.  
PA (WATA ) WATANABE C K.  
PA (WOOD ) WOOD W L.  
Query Match 100.0%; Score 3502; DB 10; Length 678;  
Best Local Similarity 100.0%; Pred. No. 1.1e-306;  
RESULT 667  
ID ADB85607 standard; protein: 678 AA.  
DE Novel human secreted and transmembrane protein PRO1277.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.7%; Score 3493; DB 7; Length 678;  
Best Local Similarity 99.9%; Pred. No. 7.3e-306;  
RESULT 668  
ID ADJ70701 standard; protein: 693 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID2507.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO ) MITOKOR.  
PA (BUCK ) BUCK INST AGE RES.  
Query Match 99.5%; Score 3484.5; DB 7; Length 693;  
Best Local Similarity 97.8%; Pred. No. 4.5e-305;  
RESULT 669  
ID AAB08815 standard; protein: 656 AA.  
DE Amino acid sequence of a human vitrin polypeptide.  
PN CA2255477-A1.  
PD 11-JUN-2000.  
PA (UABR ) UAB RES FOUND.  
Query Match 95.5%; Score 3344; DB 3; Length 656;  
Best Local Similarity 96.0%; Pred. No. 2e-292;  
RESULT 670  
ID ABG73355 standard; protein: 656 AA.  
DE Human ocular vitreous protein (vitrin).  
PN US2002160937-A1.  
PD 31-OCT-2002.  
PA (MAYN ) MAYNE R.  
PA (RENZ ) REN Z.  
PA (LIU ) LIU J.

Query Match 95.5%; Score 3344; DB 6; Length 656;  
Best Local Similarity 96.0%; Pred. No. 2e-292;  
RESULT 671  
ID ABM84763 standard; protein: 614 AA.  
DE Human diagnostic and therapeutic protein SEQ ID NO:5012.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY ) INCYTE CORP.  
Query Match 89.5%; Score 3136; DB 8; Length 614;  
Best Local Similarity 90.6%; Pred. No. 1.2e-273;  
RESULT 672  
ID ABB97508 standard; protein: 509 AA.  
DE Novel human protein SEQ ID NO: 776.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE ) HYSEQ INC.  
Query Match 72.4%; Score 2534.5; DB 5; Length 509;  
Best Local Similarity 97.1%; Pred. No. 2e-219;  
RESULT 673  
ID AAB85100 standard; protein: 329 AA.  
DE Human Zwfl polypeptide.  
PN WO200142466-A2.  
PD 14-JUN-2001.  
PA (ZIMO ) ZYMOGENETICS INC.  
Query Match 48.4%; Score 1695; DB 4; Length 329;  
Best Local Similarity 99.7%; Pred. No. 7.6e-144;  
RESULT 674  
ID AAO14430 standard; protein: 329 AA.  
DE Human von Willebrand factor type A domain superfamily member, Zwfl.  
PN US2002004228-A1.  
PD 10-JAN-2002.  
PA (HOLL ) HOLLOWAY J L.  
Query Match 48.4%; Score 1695; DB 5; Length 329;  
Best Local Similarity 99.7%; Pred. No. 7.6e-144;  
RESULT 675  
ID ADF67846 standard; protein: 329 AA.  
DE Human Zwfl.  
PN US2003077751-A1.  
PD 24-APR-2003.  
PA (HOLL ) HOLLOWAY J L.  
Query Match 48.4%; Score 1695; DB 7; Length 329;  
Best Local Similarity 99.7%; Pred. No. 7.6e-144;  
RESULT 676  
ID ADP29321 standard; protein: 531 AA.  
DE Human secreted protein SEQ ID #1319.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE ) FIVE PRIME THERAPEUTICS INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 531;  
Best Local Similarity 36.9%; Pred. No. 1.8e-92;  
RESULT 677  
ID AAY13383 standard; protein: 550 AA.  
DE Amino acid sequence of protein PRO294.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 2; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 678  
ID AAY84405 standard; protein: 550 AA.  
DE Amino acid sequence of human COCH5h2 polypeptide.  
PN WO200018211-A2.  
PD 06-APR-2000.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 32.3%; Score 1129.5; DB 3; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 679  
ID AAB80251 standard; protein: 550 AA.  
DE Human PRO294 protein.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 4; Length 550;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 680  
 ID AAB50429 standard; protein; 550 AA.  
 DE Human COCH5B2 protein.  
 PN WO200071081-A2.  
 PD 30-NOV-2000.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 32.3%; Score 1129.5; DB 4; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 681  
 ID AAU29046 standard; protein; 550 AA.  
 DE Human PRO polypeptide sequence #23.  
 PN WO200168848-A2.  
 PD 20-SEP-2001.  
 PA (GETH) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 4; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 682  
 ID ABUS8422 standard; protein; 550 AA.  
 DE Human PRO polypeptide #23.  
 PN US2003027272-A1.  
 PD 06-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 683  
 ID ABU71629 standard; protein; 550 AA.  
 DE Human PRO polypeptide #40.  
 PN US2002146709-A1.  
 PD 10-OCT-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 684  
 ID ABU87970 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003032127-A1.  
 PD 13-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 685  
 ID ABU84285 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003032112-A1.  
 PD 13-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 686  
 ID ABR66159 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003027278-A1.  
 PD 06-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 687  
 ID ABR65549 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003036159-A1.  
 PD 20-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 688  
 ID ABU99489 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003040070-A1.  
 PD 27-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 689  
 ID ABU82728 standard; protein; 550 AA.  
 DE Human PRO polypeptide #23.  
 PN US2003032113-A1.  
 PD 13-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 690  
 ID ABU98949 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003036147-A1.  
 PD 20-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 691  
 ID ABU71484 standard; protein; 550 AA.  
 DE Human PRO polypeptide #40.  
 PN US2002192659-A1.  
 PD 19-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 692  
 ID ABR68098 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003027264-A1.  
 PD 06-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 693  
 ID ABU96151 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003036144-A1.  
 PD 20-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 694  
 ID ABU92582 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003036149-A1.  
 PD 20-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 695  
 ID ABO08659 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003044923-A1.  
 PD 06-MAR-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 696  
 ID ABO02711 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003040062-A1.  
 PD 27-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 697  
 ID ABR74865 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003040056-A1.  
 PD 27-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 698  
 ID ABR94627 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003044926-A1.  
 PD 06-MAR-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 699  
 ID ABU85600 standard; protein; 550 AA.  
 DE Human PRO polypeptide #23.  
 PN US2003036140-A1.  
 PD 20-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;

RESULT 700  
 ID ABU98760 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003013153-A1.  
 PD 16-JAN-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 701  
 ID ABU97975 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003017544-A1.  
 PD 23-JAN-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 702  
 ID ABU91681 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003027277-A1.  
 PD 06-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 703  
 ID ABU71930 standard; protein; 550 AA.  
 DE Human secreted/cransmembrane protein PRO294.  
 PN US2003003530-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 704  
 ID ABU89374 standard; protein; 550 AA.  
 DE Human PRO polypeptide #23.  
 PN US2003036141-A1.  
 PD 20-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 705  
 ID ABU86215 standard; protein; 550 AA.  
 DE Human secreted/cransmembrane protein (PRO) #23.  
 PN US2003036146-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 706  
 ID ABU67428 standard; protein; 550 AA.  
 DE Human secreted/cransmembrane protein (PRO) #23.  
 PN US2003036162-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 707  
 ID ABU80456 standard; protein; 550 AA.  
 DE Human PRO protein #23.  
 PN US2003036137-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 708  
 ID ABO01813 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2002197671-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 709  
 ID ABR9374 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SRQ ID NO:46.  
 PN US2003040063-A1.  
 PD 27-FEB-2003.

Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 710  
 ID ABR98764 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003040064-A1.  
 PD 27-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 711  
 ID ABO16287 standard; protein; 550 AA.  
 DE Human secreted/cransmembrane protein (PRO) #23.  
 PN US2003027267-A1.  
 PD 06-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 712  
 ID ABR92187 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003036160-A1.  
 PD 20-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 713  
 ID ABO18828 standard; protein; 550 AA.  
 DE Human secreted/cransmembrane protein (PRO) #23.  
 PN US2003044925-A1.  
 PD 06-MAR-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 714  
 ID ABR78249 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003054474-A1.  
 PD 20-MAR-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 715  
 ID ABU84985 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003032114-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 716  
 ID ABO00124 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003032101-A1.  
 PD 13-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 717  
 ID ABO11456 standard; protein; 550 AA.  
 DE Human secreted/cransmembrane protein (PRO) #23.  
 PN US2003036124-A1.  
 PD 20-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 718  
 ID ABO02101 standard; protein; 550 AA.  
 DE Human secreted/cransmembrane protein (PRO) #23.  
 PN US2003040054-A1.  
 PD 27-FEB-2003.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 719  
 ID ABU54386 standard; protein; 550 AA.  
 DE Human secreted/cransmembrane protein PRO294.  
 PN US2002132240-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 720  
ID ABU98675 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 721  
ID ABU83370 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 722  
ID AB006171 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 723  
ID ABR59207 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 724  
ID ABO09269 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 725  
ID ABO19133 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 726  
ID ABO1151 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 727  
ID ABR66769 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 728  
ID ABO15982 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 729  
ID ABO13688 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 730  
ID ABO07744 standard; protein; 550 AA.

ID ABO47401 standard; protein; 550 AA.  
DE Human secreted/transmembrane polypeptide PRO294.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 731  
ID ABU65591 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, SEQ ID 46.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 732  
ID ABO07439 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 733  
ID ABO03626 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 734  
ID ABR67074 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 735  
ID ABO15677 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 736  
ID ABU5958 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, PRO294.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 737  
ID ABU65286 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 738  
ID ABR95231 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 739  
ID ABU71134 standard; protein; 550 AA.  
DE Human PRO294 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 740  
ID ABO07744 standard; protein; 550 AA.

DE Human PRO polypeptide #23.  
PN US200302130-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 741  
ID ABR69985 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 742  
ID ABR69318 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 743  
ID ABO01459 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 744  
ID ABU81261 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 745  
ID ABR60058 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 746  
ID ABR67793 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 747  
ID ABR65181 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 748  
ID ABR68403 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 749  
ID ABR71815 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 750  
ID ABU85295 standard; protein; 550 AA.

DE Human PRO polypeptide #23.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 751  
ID ABU8985 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 752  
ID ABU83065 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 753  
ID ABU94921 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 754  
ID ABU90469 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 755  
ID ABU83980 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 756  
ID ABU93631 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 757  
ID ABR64876 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 758  
ID ABR68708 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 759  
ID ABO06524 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 760  
ID ABR99069 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040068-A1.

PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 761  
ID ABUS6953 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 762  
ID ABUS64538 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #42.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 763  
ID ABUS5905 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 764  
ID ABUS67384 standard; protein; 550 AA.  
DE Human secreted protein PRO294.  
PN US2003032054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 765  
ID ABUS82192 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 766  
ID ABUS87203 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 767  
ID ABUS83675 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 768  
ID ABUS8049 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 769  
ID ABUS14904 standard; protein; 550 AA.  
DE Human secreted / transmembrane polypeptide PRO294.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 770  
ID ABUS81760 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 771  
ID ABUS5924 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 772  
ID ABUS9753 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 773  
ID ABUS93941 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 774  
ID ABUS9794 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 775  
ID ABUS6646 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 776  
ID ABUS90882 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 777  
ID ABUS94309 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 778  
ID ABUS79191 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 779  
ID ABUS8520 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 780  
ID ABUS8625 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 781  
ID ABU94614 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 782  
ID ABO04541 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 783  
ID ABR70290 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 784  
ID ABU98455 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 785  
ID ABR65854 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 786  
ID ABR64571 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 787  
ID ABU79496 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 788  
ID ABU92887 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 789  
ID ABU95846 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 790  
ID ABU91066 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 791

ID ABU90159 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 792  
ID ABO09574 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 793  
ID ABO10846 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 794  
ID ABR70900 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 795  
ID ABU87508 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 796  
ID ABU91376 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 797  
ID ABU84590 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 798  
ID ABR69680 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 799  
ID ABU80057 standard; protein; 550 AA.  
DE Human PRO protein #23.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 800  
ID ABU69661 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 801  
ID ABU93326 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.



PN US2003017541-A1.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 802  
ID ABO09879 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 803  
ID ABO08964 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 804  
ID ABU10532 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein #23.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 805  
ID ABU95541 standard; protein: 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 806  
ID ABU96750 standard; protein: 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 807  
ID ABR70595 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 808  
ID ABO04946 standard; protein: 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 809  
ID ABO08354 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 810  
ID ABO14843 standard; protein: 550 AA.  
DE Human secreted / transmembrane polypeptide PRO294.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 811  
ID ABO05561 standard; protein: 550 AA.

DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 812  
ID ABR73950 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 813  
ID ABR95542 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 814  
ID ABR80839 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 815  
ID ABR81144 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 816  
ID ABR00840 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 817  
ID ABR88442 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 818  
ID ABR77263 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 819  
ID ABO28747 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 820  
ID ABO31492 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068725-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 821  
ID ABO07909 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 822  
ID ABO40389 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 823  
ID ABO35814 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 824  
ID ABO43953 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 825  
ID AOA77798 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 826  
ID AAM24748 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 827  
ID ADB29432 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 828  
ID ABO03016 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 829  
ID ABR90272 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 830

ID ABM17186 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 831  
ID ABR94932 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 832  
ID ABR95237 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 833  
ID ABO21475 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 834  
ID ABR97739 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 835  
ID ABR87527 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 836  
ID ABR77568 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 837  
ID ABR27798 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 838  
ID ABR06079 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 839  
ID ABR03585 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068722-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 840  
ID ABM35036 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 841  
ID ABM26273 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 842  
ID ABO48055 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 843  
ID ABR92797 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 844  
ID ABO24558 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 845  
ID ABM11569 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 846  
ID ABM02670 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 847  
ID ABM15966 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 848  
ID ABO27527 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003064451-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 849  
ID ABM29018 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 850  
ID ABM06994 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 851  
ID ABM21088 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 852  
ID ABM09434 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 853  
ID ABO41304 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 854  
ID ABO36119 standard; protein: 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 855  
ID ABO43648 standard; protein: 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 856  
ID ABM76348 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 857  
ID ABM76044 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;

Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 858			
ID ABR25663 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US200304542-A1.			
PD 05-JUN-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 859			
ID ABR25968 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US200304543-A1.			
PD 05-JUN-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 860			
ID ABO03321 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
FN US2003036127-A1.			
PD 20-FEB-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 861			
ID ABO02406 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
FN US2003040061-A1.			
PD 27-FEB-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 862			
ID ABR90577 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US2003036130-A1.			
PD 20-FEB-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 863			
ID ABR3645 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US2003054468-A1.			
PD 20-MAR-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 864			
ID ABO16897 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
FN US2003054470-A1.			
PD 20-MAR-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 865			
ID ABR94322 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US2003044917-A1.			
PD 06-MAR-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 866			
ID ABR75829 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US2003044929-A1.			
PD 06-MAR-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 867			
ID ABR18288 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein, #44.			
FN US2003039971-A1.			
PD 27-FEB-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 868			
ID ABR25663 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US200304542-A1.			
PD 05-JUN-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 859			
ID ABR25968 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US200304543-A1.			
PD 05-JUN-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 860			
ID ABO03321 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
FN US2003036127-A1.			
PD 20-FEB-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 861			
ID ABO02406 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
FN US2003040061-A1.			
PD 27-FEB-2003.			
Query Match			
Best Local Similarity	32.3%;	Score 1129.5; DB 6;	Length 550;
PD 37.1%;	Pred. No. 2.4e-92;		
RESULT 862			
ID ABR90577 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
FN US2003036130-A			

Best Local Similarity	37.1%	Pred. No. 2.4e-92;	
RESULT 868			
ID ABO32795 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein PRO294.			
PN US2003045693-A1.			
PD 06-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 869			
ID ABR71205 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003059880-A1.			
PD 27-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 870			
ID ABR93102 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003064465-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 871			
ID ABR93407 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003054478-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 872			
ID ABR87832 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003068718-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 873			
ID ABO27832 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
PN US2003064454-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 874			
ID ABO29967 standard; protein; 550 AA.			
DE Human secreted/transmembrane protein (PRO) #23.			
PN US2003064461-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 875			
ID ABO33176 standard; protein; 550 AA.			
DE Human PRO polypeptide #23.			
PN US2003068724-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 876			
ID ABO4864 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003068727-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	
RESULT 877			
ID ABO4864 standard; protein; 550 AA.			
DE Human secreted polypeptide PRO294, SEQ ID NO:46.			
PN US2003068727-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	32.3%;	Score 1129.5; DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;	

RESULT 877  
ID ABM08824 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 878  
ID ABO36424 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 879  
ID ABO35509 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 880  
ID ABO39474 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 881  
ID ABM10349 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 882  
ID ABM1874 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 883  
ID ABO52020 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 884  
ID ABO52325 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 885  
ID ABO23643 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 886  
ID ABR97129 standard; protein; 550 AA.

DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 887  
ID ABR86917 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 888  
ID ABM10959 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003045782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 889  
ID ABM28103 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 890  
ID ABO32102 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 891  
ID ABM15229 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 892  
ID ABM06384 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 893  
ID ABM04195 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 894  
ID ABM22308 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 895  
ID ABM07604 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.

PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 896  
ID ABO40694 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 897  
ID ABO35341 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 898  
ID ABO33104 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 899  
ID ABO52630 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 900  
ID ABO50190 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 901  
ID ABO99184 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 902  
ID ABO04236 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 903  
ID ABO05866 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 904  
ID ABO34655 standard; protein; 550 AA.  
DE Human PRO polypeptide #40.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;

RESULT 905  
ID ABO18406 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 906  
ID ADA16263 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 907  
ID ABR97434 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 908  
ID ABR80534 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 909  
ID ABO01145 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 910  
ID ABR88747 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 911  
ID ABO13399 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 912  
ID ABO20783 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 913  
ID ABO41914 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 914  
ID ABO42524 standard; protein; 550 AA.

DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003049751-A1.  
 ID ABR6612 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003049772-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 915

ID ABR10044 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003067478-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 916

ID ABO38559 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003068773-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 917

ID ABR32799 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003073185-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 918

ID ABR22613 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003087373-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 919

ID ABR74824 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003096353-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 920

ID ADA79590 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003073173-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 921

ID ABR96214 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003054458-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 922

ID ABR02365 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003059886-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 923

ID ABR86307 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003049758-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 924

ID ABR6612 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003049772-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 925

ID ABR16576 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003064448-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 926

ID ABR29628 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003064456-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 927

ID ABO29052 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003068693-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 928

ID ABR23833 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003068735-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 929

ID ABR3223 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003068753-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 930

ID ABR22003 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003068742-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 931

ID ABO37644 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003068756-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 932

ID ABR28408 standard; protein; 550 AA.  
 DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
 PN US2003082715-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 933

ID ABM28713 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 934  
ID ABM66357 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068737-A1.  
PD 10-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 935  
ID ABM75739 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 936  
ID ABM34019 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 937  
ID ABM34324 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 938  
ID ABO20255 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 939  
ID ABO21170 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 940  
ID ABO22085 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 941  
ID ABR96519 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 942  
ID ABR85697 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 943  
ID ABR99679 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 944  
ID ABM00230 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 945  
ID ABM00535 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 946  
ID ABO29662 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068700-A1.  
PD 10-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 947  
ID ABM23528 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068736-A1.  
PD 10-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 948  
ID ABM29323 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068679-A1.  
PD 10-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 949  
ID ABO38254 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068767-A1.  
PD 10-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 950  
ID ABO45554 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003073182-A1.  
PD 17-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 951  
ID ABM20478 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;



RESULT 952  
ID ADA42408 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 953  
ID ADA81317 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 954  
ID ABO16592 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 955  
ID ABO18218 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 956  
ID ABO22645 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 957  
ID ABO22950 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 958  
ID ABR92492 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 959  
ID ABR81449 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 960  
ID ABO17533 standard; protein; 550 AA.  
DE Human PRO polypeptide #40.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 961  
ID ABR77873 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049783-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 962  
ID ABR89662 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 963  
ID ABR26578 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 964  
ID ABR13704 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 965  
ID ABO28442 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 966  
ID ABO30272 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 967  
ID ABR07299 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 968  
ID ABR03890 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 969  
ID ABO37034 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 970  
ID ABO41609 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 971  
ID ABR77873 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049783-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;

Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 971  
ID ABO35204 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 972  
ID ABM25053 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 973  
ID ABO47445 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 974  
ID ABO47750 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 975  
ID ABO48360 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 976  
ID ABO51410 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 977  
ID ABO51715 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 978  
ID ABO50495 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 979  
ID ABR79619 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 980  
ID ABM16881 standard; protein; 550 AA.  
PA (GETH ) GENENTECH INC.

DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 981  
ID ABO17913 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 982  
ID ABO20865 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 983  
ID ABR96824 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 984  
ID ABM12179 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 985  
ID ABM16271 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 986  
ID ABM24138 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 987  
ID ABM14619 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 988  
ID ABM04500 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 989  
ID ABM06689 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 990  
ID AEM09129 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 991  
ID ABO39169 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 992  
ID ABR75434 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 993  
ID ABR25358 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 994  
ID ABR19868 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 995  
ID ABO46774 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 996  
ID ABO47079 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 997  
ID ADA83115 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 998  
ID ABR71510 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 999  
ID ABR72120 standard; protein; 550 AA.

DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1000  
ID ABR98459 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1001  
ID ABO06829 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1002  
ID ABR84782 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1003  
ID ABR73340 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1004  
ID ABR76434 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1005  
ID ABR73035 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1006  
ID ABR18101 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1007  
ID ABO20560 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1008  
ID ABO25303 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1009  
ID ABO25608 standard; protein; 550 AA.

DE Human PRO polypeptide #23.  
PD US2003054466-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1010  
ID ABR94017 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003059879-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1011  
ID ABR79924 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003049738-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1012  
ID ABR11264 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1013  
ID ABO32871 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PD US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1014  
ID ABO30577 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PD US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1015  
ID ABO30882 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PD US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1016  
ID ABR7188 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1017  
ID ABR29933 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1018  
ID ABR05469 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003045700-A1.

PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1019  
ID ABR15534 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1020  
ID ABR08519 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1021  
ID ABR042219 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PD US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1022  
ID ABR037949 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PD US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1023  
ID ABR045859 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PD US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1024  
ID ABR66662 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1025  
ID ABR20158 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PD US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1026  
ID ABR19563 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PD US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 6; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1027  
ID ABR049275 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PD US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match	32.3%;	Score 1129.5;	DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1028				
ID ABO49580 standard; protein; 550 AA.				
DE Human secreted/transmembrane protein (PRO) #23.				
PN US2003049775-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	32.3%;	Score 1129.5;	DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1029				
ID ADA78410 standard; protein; 550 AA.				
DE Human secreted/transmembrane protein (PRO) #23.				
PN US2003073181-A1.				
PD 17-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	32.3%;	Score 1129.5;	DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1030				
ID ABR88137 standard; protein; 550 AA.				
DE Human secreted polypeptide PRO294, SEQ ID NO:46.				
PN US2003068720-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	32.3%;	Score 1129.5;	DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1031				
ID ABM26883 standard; protein; 550 AA.				
DE Human secreted polypeptide PRO294, SEQ ID NO:46.				
PN US2003068739-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	32.3%;	Score 1129.5;	DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1032				
ID ABM03280 standard; protein; 550 AA.				
DE Human secreted polypeptide PRO294, SEQ ID NO:46.				
PN US2003068763-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	32.3%;	Score 1129.5;	DB 6;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1033				
ID ABO39779 standard; protein; 550 AA.				
DE Human secreted/transmembrane protein (PRO) #23.				
PN US2003068689-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	32.3%;	Score 1129.5;	DB 7;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1034				
ID ABO49885 standard; protein; 550 AA.				
DE Human secreted/transmembrane protein (PRO) #23.				
PN US2003049776-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	32.3%;	Score 1129.5;	DB 7;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1035				
ID ABO50800 standard; protein; 550 AA.				
DE Human secreted/transmembrane protein (PRO) #23.				
PN US2003049780-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	32.3%;	Score 1129.5;	DB 7;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
RESULT 1036				
ID ABO05256 standard; protein; 550 AA.				
DE Human secreted/transmembrane protein (PRO) #23.				
PN US2003036126-A1.				
PD 20-FEB-2003.				
Query Match	32.3%;	Score 1129.5;	DB 7;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
Query Match	32.3%;	Score 1129.5;	DB 7;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		
Query Match	32.3%;	Score 1129.5;	DB 7;	Length 550;
Best Local Similarity	37.1%;	Pred. No. 2.4e-92;		

```

RESULT 1037
ID ABR74560 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003044524-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1038
ID ABR77039 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1039
ID ADA16687 standard; protein: 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003039969-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1040
ID ABA117796 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1041
ID ABA95847 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1042
ID ADA13116 standard; protein: 550 AA.
DE Human secreted/transmembrane protein, #44.
PN US2003049622-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1043
ID ABA021780 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003054475-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1044
ID ABA019950 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1045
ID ABA024253 standard; protein: 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003064467-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1046
ID ABA886002 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003048759-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;
RESULT 1047
ID ABA886002 standard; protein: 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003048759-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;
Pred. No. 2.4e-92;

```

Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1047  
ID ABO10654 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1048  
ID ABO76653 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1049  
ID ABR89357 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1050  
ID ABO12484 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1051  
ID ABO05774 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1052  
ID ABO34899 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1053  
ID ABO02975 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1054  
ID ABO18953 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1055  
ID ABO19258 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1056  
ID ABO19258 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;

RESULT 1056  
ID ABO46469 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1057  
ID ABO48970 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1058  
ID ABO41984 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1059  
ID ABO69013 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1060  
ID ABR89052 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1061  
ID ABR72425 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1062  
ID ABR74255 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1063  
ID ABO18523 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1064  
ID ADA17331 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1065  
ID ABR80229 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049739-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1066  
ID ABM01450 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1067  
ID ABM02060 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1068  
ID ABR87222 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1069  
ID ABM12789 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1070  
ID ABM30543 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1071  
ID ABM24443 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1072  
ID ABO29357 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1073  
ID ABO31187 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1074  
ID ABM14314 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1075  
ID ABM09739 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1076  
ID ABO38864 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1077  
ID ABM34629 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1078  
ID ABO51105 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1079  
ID ADA42834 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1080  
ID ABO03931 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1081  
ID ABO10401 standard; protein: 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1082  
ID ABR77644 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1083  
ID ABR78854 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1084  
ID ABO23948 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003054482-A1.

```
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1085
ID ABR93712 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1086
ID ABM01755 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1087
ID ABM78178 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1088
ID ABR89967 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1089
ID ABM27493 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1090
ID ABM13094 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1091
ID ABO31797 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1092
ID ABM14009 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1093
ID ABM08214 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1094
ID ABO40084 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1095
ID ABM74519 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1096
ID ABM33714 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1097
ID ABM20173 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1098
ID ABO48665 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1099
ID ABR72730 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1100
ID ABO15372 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1101
ID ABR85087 standard; protein; 550 AA.
DE Human secreted polypeptide PRO294, SEQ ID NO:46.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1102
ID ABO15067 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 32.3%; Score 1129.5; DB 7; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.4e-92;
RESULT 1103
ID ABO17202 standard; protein; 550 AA.
DE Human secreted/transmembrane protein (PRO) #23.
```



PN US2003040077-A1.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1104  
ID ABM17491 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1105  
ID ABR85392 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1106  
ID ABO17594 standard; protein: 550 AA.  
DE Human PRO polypeptide #40.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1107  
ID ABW76958 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1108  
ID ABO28137 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1109  
ID ABM22918 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1110  
ID ABM30238 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1111  
ID AAM21698 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1112  
ID AAM21393 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1113  
ID ABM14924 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1114  
ID ABO40999 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1115  
ID ABO36729 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1116  
ID ABO37339 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1117  
ID ABW5129 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1118  
ID ABM33409 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1119  
ID ABO46164 standard; protein: 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1120  
ID ADA82481 standard; protein: 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1121  
ID ABM31763 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 32.3%; Score 1129.5; DB 7; Length 550;  
37.1%; Pred. No. 2.4e-92;  
RESULT 1122  
ID AAM31763 standard; protein: 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

RESULT 1122  
ID ADM31153 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1123  
ID ADM77753 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1124  
ID ADM74889 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1125  
ID ADM85789 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1126  
ID ADM32068 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1127  
ID ADM32373 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1128  
ID ADM31458 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1129  
ID ADM30848 standard; protein; 550 AA.  
DE Human secreted polypeptide PRO294, SEQ ID NO:46.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1130  
ID ADC28535 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1131

ID ADC39735 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1132  
ID ADC40249 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1133  
ID ADC19073 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1134  
ID ADC34373 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1135  
ID ADC29428 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003048676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1136  
ID ADC28959 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1137  
ID ADC40844 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1138  
ID ADC19501 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1139  
ID ADC33949 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1140  
ID ADC13019 standard; protein; 550 AA.

DE Human secreted/transmembrane protein, #44.  
 PN US2003073079-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1141  
 ID ADG12471 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003082541-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1142  
 ID ADD05519 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein (PRO) #23.  
 PN US2003087376-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1143  
 ID ADD05026 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003104469-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1144  
 ID ADD04032 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003104381-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1145  
 ID ADD03608 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003108983-A1.  
 PD 12-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1146  
 ID ADD34860 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003077583-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1147  
 ID ADD02514 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003207397-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1148  
 ID ADD01221 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003207399-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1149  
 ID ADP95396 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.

PN US2003207398-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1150  
 ID ADG12211 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003207392-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1151  
 ID ADH08871 standard; protein; 550 AA.  
 DE Human PRO polypeptide #23.  
 PN US2003207395-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1152  
 ID ADH59343 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003039972-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1153  
 ID ADI38122 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003054352-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1154  
 ID ADJ26390 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003054349-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1155  
 ID ADI32652 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003207396-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1156  
 ID ADM30186 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2003073813-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 7; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1157  
 ID ADE79305 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003135025-A1.  
 PD 17-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1158  
 ID ADE79729 standard; protein; 550 AA.  
 DE Human secreted/transmembrane protein, #44.  
 PN US2003130489-A1.  
 PD 10-JUL-2003.

PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1159  
ID ADEB73405 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1160  
ID ADEB74183 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1161  
ID ADEB73940 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1162  
ID ADEB74795 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein (PRO) #23.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1163  
ID ADEB99494 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1164  
ID ADEB98613 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1165  
ID ADEB99040 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1166  
ID ADG40510 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILT/) WILTAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1167  
ID ADF73904 standard; protein; 550 AA.

DE Human secreted/transmembrane protein, #44.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1168  
ID ADF96008 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1169  
ID ADF73480 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1170  
ID ADG04279 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1171  
ID ADG00439 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1172  
ID ADG82695 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1173  
ID ADG92323 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1174  
ID ADG92750 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1175  
ID ADH25976 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1176  
ID ADH32945 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2003068768-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1177  
ID ADH20539 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1178  
ID ADH07394 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2004006211-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODO/) GODDARD A. J.  
PA (GODN/) GODOWSKI P. J.  
PA (GURN/) GURNEY A. L.  
PA (MATH/) MATHER J. P.  
PA (WILL/) WILLIAMS P. M.  
PA (WOOD/) WOOD W. I.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1179  
ID ADH59939 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003215904-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1180  
ID ADH06567 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODO/) GODDARD A. J.  
PA (GODN/) GODOWSKI P. J.  
PA (GURN/) GURNEY A. L.  
PA (MATH/) MATHER J. P.  
PA (WILL/) WILLIAMS P. M.  
PA (WOOD/) WOOD W. I.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1181  
ID ADI18709 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003152999-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1182  
ID ADI65429 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1183  
ID ADI37688 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1184

ID ADH97488 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003190610-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1185  
ID ADI65856 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003148371-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1186  
ID ADH60599 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2004023331-A1.  
PD 05-FEB-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODO/) GODDARD A. J.  
PA (GODN/) GODOWSKI P. J.  
PA (GURN/) GURNEY A. L.  
PA (MATH/) MATHER J. P.  
PA (WILL/) WILLIAMS P. M.  
PA (WOOD/) WOOD W. I.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1187  
ID ADI20064 standard; protein; 550 AA.  
DE Protein #1 of the invention.  
PN WO2004003020-A1.  
PD 08-JAN-2004.  
PA (NIME-) NIPPON MEDICAL SCHOOL FOUND.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1188  
ID ADJ99656 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003187238-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1189  
ID ADI08849 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1190  
ID ADJ54684 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1191  
ID ADW25190 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1192  
ID ADM29940 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PN US2003190611-A1.

PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1193  
ID ADJ64455 standard; protein; 550 AA.  
DE Human PRO polypeptide #23.  
PD US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1194  
ID ADM31351 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PD US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1195  
ID ADM36398 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PD US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1196  
ID ADM40203 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PD US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1197  
ID ADO06262 standard; protein; 550 AA.  
DE Human PRO polypeptide #40.  
PD US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1198  
ID ADN37811 standard; protein; 550 AA.  
DE Novel human secreted and transmembrane protein PRO294.  
PD US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1199  
ID ADR11114 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PD US2004137561-A1.  
PD 15-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1200  
ID ADR18023 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PD US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (BATC/) BATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.

PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANT/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1201  
ID ADS74662 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein #44.  
PD US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) BATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODD/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANT/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1202  
ID ADT03699 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PD US2003152922-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1203  
ID ADU06473 standard; protein; 550 AA.  
DE Novel bronchial cancer-associated human protein SegID697.  
PD DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
Query Match 32.3%; Score 1129.5; DB 8; Length 550;  
Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
RESULT 1204  
ID AEA37937 standard; protein; 550 AA.  
DE Human secreted/transmembrane protein, #44.  
PD US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.

Query Match 32.3%; Score 1129.5; DB 9; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1205  
 ID AED23971 standard; protein; 550 AA.  
 DE Human secreted protein PRO 294, SEQ ID 227.  
 PN US2005214904-A1.  
 PD 29-SEP-2005.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 9; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1206  
 ID AED50041 standard; protein; 550 AA.  
 DE Novel human secreted and transmembrane protein PRO294.  
 PN US2005163766-A1.  
 PD 28-JUL-2005.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 9; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1207  
 ID AEB69140 standard; protein; 550 AA.  
 DE Collagen homologous PRO294 protein, SEQ ID 227.  
 PN US6974689-B1.  
 PD 13-DEC-2005.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.3%; Score 1129.5; DB 10; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 2.4e-92;  
 RESULT 1208  
 ID ADO41974 standard; protein; 615 AA.  
 DE Human cell adhesion and extracellular matrix protein 3 SeqID3.  
 PN WO2004048529-A2.  
 PD 10-JUN-2004.  
 PA (INCYT-) INCYTE CORP.  
 Query Match 32.2%; Score 1127.5; DB 8; Length 615;  
 Best Local Similarity 37.1%; Pred. No. 4.3e-92;  
 RESULT 1209  
 ID ADC78547 standard; protein; 550 AA.  
 DE Human PRO294 protein.  
 PN WO20015796-A2.  
 PD 23-MAR-2000.  
 PA (GETH ) GENENTECH INC.  
 Query Match 32.2%; Score 1126.5; DB 3; Length 550;  
 Best Local Similarity 37.1%; Pred. No. 4.4e-92;  
 RESULT 1210  
 ID AAB50430 standard; protein; 550 AA.  
 DE Human mutant COCH5B2 protein.  
 PN WO200071081-A2.  
 PD 30-NOV-2000.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 32.0%; Score 1121.5; DB 4; Length 550;  
 Best Local Similarity 36.9%; Pred. No. 1.3e-91;  
 RESULT 1211  
 ID AAY84406 standard; protein; 552 AA.  
 DE Amino acid sequence of a murine COCH5B2 polypeptide.  
 PN WO200018211-A2.  
 PD 06-APR-2000.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 31.8%; Score 1113; DB 3; Length 552;  
 Best Local Similarity 36.2%; Pred. No. 7.4e-91;  
 RESULT 1212  
 ID AEA90324 standard; protein; 432 AA.  
 DE Human NOV12a SEQ ID NO 32.  
 PN WO2003064629-A2.  
 PD 07-AUG-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 27.7%; Score 969.5; DB 7; Length 432;  
 Best Local Similarity 44.4%; Pred. No. 4.6e-76;  
 RESULT 1213  
 ID AAB08817 standard; protein; 178 AA.  
 DE A von Willebrand A domain derived from a human vitrin polypeptide.  
 PN CA2255477-A1.  
 PD 11-JUN-2000.  
 PA (UABR-) UAB RES FOUND.  
 Query Match 26.1%; Score 915; DB 3; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-74;

RESULT 1214  
 ID ADR41420 standard; protein; 204 AA.  
 DE Human CD-like molecule HACAD35, SEQ ID NO:219.  
 PN WO200226930-A2.  
 PD 04-APR-2002.  
 PA (HOMA-) HUMAN GENOME SCI INC.  
 Query Match 25.8%; Score 904.5; DB 5; Length 204;  
 Best Local Similarity 90.5%; Pred. No. 9.9e-73;  
 RESULT 1215  
 ID AAM17950 standard; protein; 172 AA.  
 DE Peptide #4384 encoded by probe for measuring cervical gene expression.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 25.6%; Score 898; DB 4; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-72;  
 RESULT 1216  
 ID ABB36981 standard; peptide; 172 AA.  
 DE Peptide #4487 encoded by human foetal liver single exon probe.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 25.6%; Score 898; DB 4; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-72;  
 RESULT 1217  
 ID AAM13577 standard; protein; 171 AA.  
 DE Peptide #11 encoded by probe for measuring cervical gene expression.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 25.5%; Score 892; DB 4; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
 RESULT 1218  
 ID ABB32505 standard; peptide; 171 AA.  
 DE Peptide #11 encoded by human foetal liver single exon nucleic acid probe.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 25.5%; Score 892; DB 4; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
 RESULT 1219  
 ID AAM2974 standard; protein; 171 AA.  
 DE Peptide #11 encoded by probe for measuring placental gene expression.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 25.5%; Score 892; DB 4; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
 RESULT 1220  
 ID ABB27360 standard; peptide; 171 AA.  
 DE Human peptide #11 encoded by breast cell single exon nucleic acid probe.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 25.5%; Score 892; DB 4; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
 RESULT 1221  
 ID ABB18012 standard; protein; 171 AA.  
 DE Protein #11 encoded by probe for measuring heart cell gene expression.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 25.5%; Score 892; DB 4; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
 RESULT 1222  
 ID AAM65717 standard; protein; 171 AA.  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26023.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 25.5%; Score 892; DB 4; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
 RESULT 1223

ID AAM53340 standard; protein; 171 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25445.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 25.5%; Score 892; DB 4; Length 171;  
Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
RESULT 1224  
ID ABG47358 standard; peptide; 171 AA.  
DE Human liver peptide, SEQ ID No 26006.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 25.5%; Score 892; DB 4; Length 171;  
Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
RESULT 1225  
ID AAM01329 standard; protein; 171 AA.  
DE Peptide #11 encoded by probe for measuring human breast gene expression.  
PN W0200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 25.5%; Score 892; DB 4; Length 171;  
Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
RESULT 1226  
ID ABG3347 standard; peptide; 171 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25012.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 25.5%; Score 892; DB 5; Length 171;  
Best Local Similarity 100.0%; Pred. No. 9.9e-72;  
RESULT 1227  
ID AAU19651 standard; protein; 186 AA.  
DE Human novel extracellular matrix protein, Seq ID No 301.  
PN W0200155318-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 25.3%; Score 885; DB 4; Length 186;  
Best Local Similarity 99.4%; Pred. No. 4.9e-71;  
RESULT 1228  
ID AAU87279 standard; protein; 186 AA.  
DE Novel central nervous system protein #189.  
PN W0200155318-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 25.3%; Score 885; DB 4; Length 186;  
Best Local Similarity 99.4%; Pred. No. 4.9e-71;  
RESULT 1229  
ID ABP47871 standard; protein; 186 AA.  
DE Human polypeptide SEQ ID NO 301.  
PN US2002042386-A1.  
PD 11-APR-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 25.3%; Score 885; DB 5; Length 186;  
Best Local Similarity 99.4%; Pred. No. 4.9e-71;  
RESULT 1230  
ID ADC1083 standard; protein; 186 AA.  
DE Human extracellular matrix protein from gene 26.  
PN US2003059875-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 25.3%; Score 885; DB 7; Length 186;  
Best Local Similarity 99.4%; Pred. No. 4.9e-71;  
RESULT 1231  
ID ADI34594 standard; protein; 186 AA.  
DE Novel human protein seq id 797.  
PN US2004018969-A1.  
PD 29-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.

Query Match 25.3%; Score 885; DB 8; Length 186;  
Best Local Similarity 99.4%; Pred. No. 4.9e-71;  
RESULT 1232  
ID AAB08816 standard; protein; 160 AA.  
DE A von Willebrand A domain derived from a human vitrin polypeptide.  
PN CA225477-A1.  
PD 11-JUN-2000.  
PA (UABR-) UAB RES FOUND.  
Query Match 22.8%; Score 799; DB 3; Length 160;  
Best Local Similarity 98.8%; Pred. No. 2.3e-63;  
RESULT 1233  
ID ADU76366 standard; protein; 3067 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1618.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 15.8%; Score 552; DB 8; Length 3067;  
Best Local Similarity 27.5%; Pred. No. 6.8e-39;  
RESULT 1234  
ID ABB90762 standard; protein; 3063 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 257.  
PN W0200210217-A2.  
PD 07-FEB-2002.  
PA (UYUO-) UNIV JOHNS HOPKINS.  
Query Match 15.5%; Score 543.5; DB 5; Length 3063;  
Best Local Similarity 27.7%; Pred. No. 4e-38;  
RESULT 1235  
ID ABU54469 standard; protein; 3063 AA.  
DE Human tumour endothelial marker TEM 36.  
PN W0200283874-A2.  
PD 24-OCT-2002.  
PA (UYUO-) UNIV JOHNS HOPKINS.  
Query Match 15.5%; Score 543.5; DB 6; Length 3063;  
Best Local Similarity 27.7%; Pred. No. 4e-38;  
RESULT 1236  
ID ABR47415 standard; protein; 3063 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:61.  
PN W02003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 15.5%; Score 543.5; DB 6; Length 3063;  
Best Local Similarity 27.7%; Pred. No. 4e-38;  
RESULT 1237  
ID AAU27790 standard; protein; 3118 AA.  
DE Human full-length polypeptide sequence #115.  
PN W0200164834-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.5%; Score 543.5; DB 4; Length 3118;  
Best Local Similarity 27.7%; Pred. No. 4.1e-38;  
RESULT 1238  
ID ABR47416 standard; protein; 3063 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:63.  
PN W02003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 15.5%; Score 542.5; DB 6; Length 3063;  
Best Local Similarity 27.7%; Pred. No. 4.9e-38;  
RESULT 1239  
ID ADU75666 standard; protein; 3063 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:918.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 15.5%; Score 542.5; DB 8; Length 3063;  
Best Local Similarity 27.7%; Pred. No. 4.9e-38;  
RESULT 1240  
ID AAR57349 standard; protein; 496 AA.  
DE Human cartilage matrix protein.  
PN W09415627-A1.  
PD 21-JUL-1994.  
PA (GEHO-) GEN HOSPITAL CORP.  
Query Match 14.3%; Score 501.5; DB 2; Length 496;



Best Local Similarity 28.8%; Pred. No. 1.2e-35;  
 RESULT 1241  
 ID ADP54237 standard; protein; 2000 AA.  
 DE Human PRO protein sequence SEQ ID NO.213.  
 PN WO2004039956-A2.  
 PD 13-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 13.5%; Score 471.5; DB 8; Length 2000;  
 Best Local Similarity 30.9%; Pred. No. 6.3e-32;  
 RESULT 1242  
 ID ADY14520 standard; protein; 2000 AA.  
 DE PRO polypeptide SEQ ID NO 326.  
 PN WO2005016962-A2.  
 PD 24-FEB-2005.  
 PA (GETH ) GENENTECH INC.  
 Query Match 13.5%; Score 471.5; DB 9; Length 2000;  
 Best Local Similarity 30.9%; Pred. No. 6.3e-32;  
 RESULT 1243  
 ID ADQ39661 standard; protein; 2211 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1324.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 13.5%; Score 471.5; DB 8; Length 2211;  
 Best Local Similarity 30.9%; Pred. No. 7.5e-32;  
 RESULT 1244  
 ID ADQ39658 standard; protein; 2244 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1321.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 13.5%; Score 471.5; DB 8; Length 2244;  
 Best Local Similarity 30.9%; Pred. No. 7.7e-32;  
 RESULT 1245  
 ID ADQ39660 standard; protein; 2411 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1323.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 13.5%; Score 471.5; DB 8; Length 2411;  
 Best Local Similarity 30.9%; Pred. No. 8.6e-32;  
 RESULT 1246  
 ID ABW8256 standard; protein; 2977 AA.  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO.2815.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 13.5%; Score 471.5; DB 8; Length 2977;  
 Best Local Similarity 30.9%; Pred. No. 1.2e-31;  
 RESULT 1247  
 ID ADQ39657 standard; protein; 2977 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1320.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 13.5%; Score 471.5; DB 8; Length 2977;  
 Best Local Similarity 30.9%; Pred. No. 1.2e-31;  
 RESULT 1248  
 ID ABR39571 standard; protein; 3151 AA.  
 DE Human alpha3 collagen VI mature chain.  
 PN WO2003015615-A2.  
 PD 27-FEB-2003.  
 PA (UYBR-) UNIV BROWN RES FOUND.  
 Query Match 13.5%; Score 471.5; DB 6; Length 3151;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1249  
 ID ABB90743 standard; protein; 3173 AA.  
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 218.  
 PN WO200210217-A2.  
 PD 07-FEB-2002.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 Query Match 13.5%; Score 471.5; DB 5; Length 3173;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;

RESULT 1250  
 ID ABUS4450 standard; protein; 3173 AA.  
 DE Human tumour endothelial marker TEM 12.  
 PN WO200283874-A2.  
 PD 24-OCT-2002.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 Query Match 13.5%; Score 471.5; DB 6; Length 3173;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1251  
 ID ABR39570 standard; protein; 3176 AA.  
 DE Human alpha3 collagen VI precursor chain.  
 PN WO2003015615-A2.  
 PD 27-FEB-2003.  
 PA (UYBR-) UNIV BROWN RES FOUND.  
 Query Match 13.5%; Score 471.5; DB 6; Length 3176;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1252  
 ID ADP6255 standard; protein; 3176 AA.  
 DE Human alpha 3 type VI collagen, isoform 1 precursor.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 13.5%; Score 471.5; DB 7; Length 3176;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1253  
 ID ADQ18247 standard; protein; 3176 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1065.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 13.5%; Score 471.5; DB 8; Length 3176;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1254  
 ID ADQ29665 standard; protein; 3176 AA.  
 DE Human colorectal cancer-associated protein #20.  
 PN EP143393-A2.  
 PD 21-JUL-2004.  
 PA (FARB ) BAYER HEALTHCARE LLC.  
 Query Match 13.5%; Score 471.5; DB 8; Length 3176;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1255  
 ID ADR87616 standard; protein; 3176 AA.  
 DE Human type VI collagen alpha 3, SEQ ID 20.  
 PN WO2004075835-A2.  
 PD 10-SEP-2004.  
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 Query Match 13.5%; Score 471.5; DB 8; Length 3176;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1256  
 ID ADU06731 standard; protein; 3176 AA.  
 DE Novel bronchial cancer-associated human protein SegID957.  
 PN DE10316701-A1.  
 PD 04-NOV-2004.  
 PA (HINZ/) HINZMANN B.  
 PA (HERM/) HERMANN K.  
 PA (CAST/) HEIDEN CASTRANOS-VELEZ E.  
 Query Match 13.5%; Score 471.5; DB 8; Length 3176;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1257  
 ID ADV70236 standard; protein; 3176 AA.  
 DE Tumor-associated antigenic target polypeptide TAT475.  
 PN WO2004112829-A2.  
 PD 29-DEC-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 13.5%; Score 471.5; DB 9; Length 3176;  
 Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
 RESULT 1258  
 ID ADZ80431 standard; protein; 3176 AA.  
 DE Mature collagen alpha 3 (VI) chain SEQ ID NO 44.  
 PN WO2005040422-A2.  
 PD 06-MAY-2005.  
 PA (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS PHARMA GMBH.  
Query Match 13.5%; Score 471.5; DB 9; Length 3176;  
Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
RESULT 1259  
ID AAF69977 standard; protein; 3176 AA.  
DE Colorectal cancer-associated marker protein SEQ ID NO:155.  
PN W02006015047-A2.  
PD 09-FEB-2006.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO ) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 13.5%; Score 471.5; DB 10; Length 3176;  
Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
RESULT 1260  
ID AAM40303 standard; protein; 3177 AA.  
DE Human polypeptide SEQ ID NO 3448.  
PN W020015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.5%; Score 471.5; DB 4; Length 3177;  
Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
RESULT 1261  
ID ADO39656 standard; protein; 3177 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1319.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 13.5%; Score 471.5; DB 8; Length 3177;  
Best Local Similarity 30.9%; Pred. No. 1.4e-31;  
RESULT 1262  
ID ADZ12635 standard; protein; 499 AA.  
DE Human cancer-associated protein #43.  
PN W02005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 13.0%; Score 454; DB 9; Length 499;  
Best Local Similarity 27.0%; Pred. No. 2.4e-31;  
RESULT 1263  
ID ADZ12643 standard; protein; 499 AA.  
DE Human cancer-associated protein #47.  
PN W02005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 13.0%; Score 454; DB 9; Length 499;  
Best Local Similarity 27.0%; Pred. No. 2.4e-31;  
RESULT 1264  
ID AAM06236 standard; protein; 159 AA.  
DE Peptide #4918 encoded by probe for measuring breast gene expression.  
PN W0200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 12.9%; Score 452.5; DB 4; Length 159;  
Best Local Similarity 51.2%; Pred. No. 4.7e-32;  
RESULT 1265  
ID ADQ65418 standard; protein; 243 AA.  
DE Novel human protein sequence #391.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.8%; Score 448.5; DB 8; Length 243;  
Best Local Similarity 38.2%; Pred. No. 2.2e-31;  
RESULT 1266  
ID AAM93257 standard; protein; 540 AA.  
DE Human polypeptide, SEQ ID NO: 2705.  
PN EPI130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 12.8%; Score 447.5; DB 4; Length 540;  
Best Local Similarity 26.4%; Pred. No. 1e-30;  
RESULT 1267  
ID ADL30672 standard; protein; 540 AA.  
DE Human protein encoded by a full length cDNA clone SegID 2705.  
PN EPI1396543-A2.  
PD 10-MAR-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.8%; Score 447.5; DB 8; Length 540;  
Best Local Similarity 26.4%; Pred. No. 1e-30;  
RESULT 1268  
ID ADZ12637 standard; protein; 540 AA.  
DE Human cancer-associated protein #44.  
PN W02005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 12.7%; Score 446.5; DB 9; Length 540;  
Best Local Similarity 26.4%; Pred. No. 1.3e-30;  
RESULT 1269  
ID ADZ12641 standard; protein; 540 AA.  
DE Human cancer-associated protein #46.  
PN W02005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 12.7%; Score 446.5; DB 9; Length 540;  
Best Local Similarity 26.4%; Pred. No. 1.3e-30;  
RESULT 1270  
ID ADO39655 standard; protein; 2210 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1318.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.7%; Score 446.5; DB 8; Length 2210;  
Best Local Similarity 29.0%; Pred. No. 1.4e-29;  
RESULT 1271  
ID AAM93255 standard; protein; 558 AA.  
DE Human polypeptide, SEQ ID NO: 2701.  
PN EPI130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 12.5%; Score 436; DB 4; Length 558;  
Best Local Similarity 24.7%; Pred. No. 1.2e-29;  
RESULT 1272  
ID ADL30668 standard; protein; 558 AA.  
DE Human protein encoded by a full length cDNA clone SegID 2701.  
PN EPI1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.5%; Score 436; DB 8; Length 558;  
Best Local Similarity 24.7%; Pred. No. 1.2e-29;  
RESULT 1273  
ID ADO41980 standard; protein; 575 AA.  
DE Human cell adhesion and extracellular matrix protein 9 SegID9.  
PN W02004048529-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.5%; Score 436; DB 8; Length 575;  
Best Local Similarity 24.7%; Pred. No. 1.3e-29;  
RESULT 1274  
ID ADO41982 standard; protein; 534 AA.  
DE Human cell adhesion and extracellular matrix protein 11 SegID11.  
PN W02004048529-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.4%; Score 435.5; DB 8; Length 534;  
Best Local Similarity 25.9%; Pred. No. 1.2e-29;  
RESULT 1275  
ID ADQ19949 standard; protein; 580 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2769.  
PN W02004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 12.4%; Score 434; DB 8; Length 580;  
Best Local Similarity 24.7%; Pred. No. 1.9e-29;  
RESULT 1276  
ID ADR66966 standard; protein; 581 AA.  
DE Human cancer associated protein sequence SEQ ID NO:12.  
PN W02004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 12.4%; Score 434; DB 8; Length 581;  
 Best Local Similarity 24.7%; Pred. No. 1.9e-29;  
 RESULT 1277  
 ID ADJ12645 standard; protein; 581 AA.  
 DE Human cancer-associated protein #48.  
 PN WO2005031001-A2.  
 PD 07-APR-2005.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 12.4%; Score 434; DB 9; Length 581;  
 Best Local Similarity 24.7%; Pred. No. 1.9e-29;  
 RESULT 1278  
 ID ADJ12647 standard; protein; 581 AA.  
 DE Human cancer-associated protein #49.  
 PN WO2005031001-A2.  
 PD 07-APR-2005.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 12.4%; Score 434; DB 9; Length 581;  
 Best Local Similarity 24.7%; Pred. No. 1.9e-29;  
 RESULT 1279  
 ID ADJ12649 standard; protein; 620 AA.  
 DE Human cancer-associated protein #50.  
 PN WO2005031001-A2.  
 PD 07-APR-2005.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 12.3%; Score 431.5; DB 9; Length 620;  
 Best Local Similarity 23.7%; Pred. No. 3.7e-29;  
 RESULT 1280  
 ID ADQ39659 standard; protein; 2205 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1322.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 11.9%; Score 416.5; DB 8; Length 2205;  
 Best Local Similarity 27.8%; Pred. No. 7e-27;  
 RESULT 1281  
 ID ADQ39662 standard; protein; 2971 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1325.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 11.9%; Score 416.5; DB 8; Length 2971;  
 Best Local Similarity 27.8%; Pred. No. 1.1e-26;  
 RESULT 1282  
 ID ADR6663 standard; protein; 644 AA.  
 DE Mouse cancer associated protein sequence SEQ ID NO:9.  
 PN WO2004074321-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 11.8%; Score 412.5; DB 8; Length 644;  
 Best Local Similarity 22.6%; Pred. No. 2e-27;  
 RESULT 1283  
 ID ADJ12632 standard; protein; 644 AA.  
 DE Murine cancer-associated protein #21.  
 PN WO2005031001-A2.  
 PD 07-APR-2005.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 11.8%; Score 412.5; DB 9; Length 644;  
 Best Local Similarity 22.6%; Pred. No. 2e-27;  
 RESULT 1284  
 ID ADB64658 standard; protein; 1036 AA.  
 DE Human protein encoded by clone MESAN20027900.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 Query Match 11.8%; Score 412; DB 7; Length 1036;  
 Best Local Similarity 29.3%; Pred. No. 5e-27;  
 RESULT 1285  
 ID AAM93707 standard; protein; 488 AA.  
 DE Human polypeptide, SEQ ID NO: 3641.  
 PN EP130094-A2.  
 PD 05-SEP-2001.  
 PA (HELI-) HELIX RES INST.

Query Match 11.7%; Score 409; DB 4; Length 488;  
 Best Local Similarity 26.0%; Pred. No. 2.6e-27;  
 RESULT 1286  
 ID ADJ1608 standard; protein; 488 AA.  
 DE Human protein encoded by a full length cDNA clone SeqID 3641.  
 PN EP1396543-A2.  
 PD 10-MAR-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 11.7%; Score 409; DB 8; Length 488;  
 Best Local Similarity 26.0%; Pred. No. 2.6e-27;  
 RESULT 1287  
 ID AAM18620 standard; protein; 75 AA.  
 DE Peptide #5054 encoded by probe for measuring cervical gene expression.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 RESULT 1288  
 ID AAM13573 standard; protein; 75 AA.  
 DE Peptide #7 encoded by probe for measuring cervical gene expression.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 RESULT 1289  
 ID ABB32501 standard; peptide; 75 AA.  
 DE Peptide #7 encoded by human foetal liver single exon nucleic acid probe.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 RESULT 1290  
 ID ABB37861 standard; peptide; 75 AA.  
 DE Peptide #5367 encoded by human foetal liver single exon probe.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 RESULT 1291  
 ID AAM25970 standard; protein; 75 AA.  
 DE Peptide #7 encoded by probe for measuring placental gene expression.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 RESULT 1292  
 ID AAM31267 standard; protein; 75 AA.  
 DE Peptide #5304 encoded by probe for measuring placental gene expression.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 RESULT 1293  
 ID ABB27356 standard; peptide; 75 AA.  
 DE Human peptide #7 encoded by breast cell single exon nucleic acid probe.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 RESULT 1294  
 ID ABB18008 standard; protein; 75 AA.  
 DE Protein #7 encoded by probe for measuring heart cell gene expression.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 RESULT 1295  
 ID ABB18008 standard; protein; 75 AA.  
 DE Protein #7 encoded by probe for measuring heart cell gene expression.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 10.9%; Score 382; DB 4; Length 75;

Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1295  
ID ABB23120 standard; protein; 75 AA.  
DE Protein #5119 encoded by probe for measuring heart cell gene expression.  
PN W0200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 4; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1296  
ID AAM65713 standard; protein; 75 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26019.  
PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 4; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1297  
ID AAM70991 standard; protein; 75 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31297.  
PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 4; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1298  
ID AAM5336 standard; protein; 75 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25441.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 4; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1299  
ID AAM58308 standard; protein; 75 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30413.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 4; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1300  
ID ABG47354 standard; peptide; 75 AA.  
DE Human liver peptide, SEQ ID No 26002.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 4; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1301  
ID ABG52707 standard; peptide; 75 AA.  
DE Human liver peptide, SEQ ID No 31355.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 4; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1302  
ID AAM01325 standard; protein; 75 AA.  
DE Peptide #7 encoded by probe for measuring human breast gene expression.  
PN W0200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 4; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1303  
ID ABG40779 standard; peptide; 75 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 30444.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 5; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;

RESULT 1304  
ID ABG35343 standard; peptide; 75 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25008.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 10.9%; Score 382; DB 5; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
RESULT 1305  
ID AB10550 standard; protein; 896 AA.  
DE Human NOV4b protein.  
PN W0200246408-A2.  
PD 13-JUN-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.9%; Score 380; DB 5; Length 896;  
Best Local Similarity 18.2%; Pred. No. 3.1e-24;  
RESULT 1306  
ID ADH17468 standard; protein; 896 AA.  
DE Human NOV13g protein - SEQ ID 158.  
PN W02003093432-A2.  
PD 13-NOV-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.9%; Score 380; DB 8; Length 896;  
Best Local Similarity 18.2%; Pred. No. 3.1e-24;  
RESULT 1307  
ID ADF30532 standard; protein; 2657 AA.  
DE Mouse angiogenesis modulating protein #8.  
PN US2003162706-A1.  
PD 28-AUG-2003.  
PA (PROCT & GAMBLE CO.  
Query Match 10.8%; Score 378; DB 7; Length 2657;  
Best Local Similarity 26.2%; Pred. No. 2.9e-23;  
RESULT 1308  
ID AAY13350 standard; protein; 915 AA.  
DE Amino acid sequence of protein PRO219.  
PN W09914328-A2.  
PD 25-MAR-1999.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 2; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1309  
ID AAY95340 standard; protein; 915 AA.  
DE Human PRO219 antitumour protein.  
PN W0200037638-A2.  
PD 29-JUN-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 3; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1310  
ID ADC78354 standard; protein; 915 AA.  
DE Human PRO219 protein.  
PN W0200015796-A2.  
PD 23-MAR-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 3; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1311  
ID AAB80218 standard; protein; 915 AA.  
DE Human PRO219 protein.  
PN W0200104311-A1.  
PD 18-JAN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 4; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1312  
ID AAU12318 standard; protein; 915 AA.  
DE Human PRO219 polypeptide sequence.  
PN W0200140466-A2.  
PD 07-JUN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 4; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1313

ID AAB53077 standard; protein; 915 AA.  
DE Human angiogenesis-associated protein PRO219, SEQ ID NO:67.  
PN WO200053753-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 4; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1314  
ID ABU71596 standard; protein; 915 AA.  
DE Human PRO polypeptide #7.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1315  
ID ABO17762 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1316  
ID ABU71451 standard; protein; 915 AA.  
DE Human PRO polypeptide #7.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1317  
ID ABU81016 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1318  
ID ABU71697 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein PRO219.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1319  
ID ABO01780 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1320  
ID ABU66716 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1321  
ID ABU54353 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein PRO219.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1322  
ID ABO47368 standard; protein; 915 AA.

DE Human secreted/transmembrane polypeptide PRO219.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1323  
ID ABU59797 standard; protein; 915 AA.  
DE Novel secreted and transmembrane protein PRO219.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1324  
ID ABO24987 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein (PRO) #147.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1325  
ID ABU64505 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1326  
ID ABU67351 standard; protein; 915 AA.  
DE Human secreted protein PRO219.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1327  
ID ABO14871 standard; protein; 915 AA.  
DE Human secreted / transmembrane polypeptide PRO219.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1328  
ID ABU66992 standard; protein; 915 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 294.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1329  
ID ABU69628 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1330  
ID ABO14810 standard; protein; 915 AA.  
DE Human secreted / transmembrane polypeptide PRO219.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1331  
ID ADA45613 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.

PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1332  
ID ADA76244 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1333  
ID ADB29239 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1334  
ID ADA18894 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1335  
ID ADB61517 standard; protein; 915 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1336  
ID ADB19302 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1337  
ID ADB27843 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1338  
ID ADA86322 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1339  
ID ADB15886 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1340  
ID ADA47672 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003073215-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1341  
ID ADA18095 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1342  
ID ABO32762 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein PRO219.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1343  
ID ADA67467 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1344  
ID ADB30474 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1345  
ID ADA85770 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1346  
ID ADA96982 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1347  
ID ADA79286 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1348  
ID ADA87425 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1349  
ID ADB16627 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003087349-A1.  
PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1350  
ID ABO34822 standard; protein; 915 AA.  
DE Human PRO polypeptide #7.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1351  
ID ADA16070 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1352  
ID ADA91719 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1353  
ID ADA14782 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1354  
ID ADA18743 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1355  
ID ADA93958 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1356  
ID ADB19854 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082891-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1357  
ID ADB13166 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1358  
ID ABO43295 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1359  
ID ADA74420 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1360  
ID ADA42215 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1361  
ID ADB24653 standard; protein; 915 AA.  
DE Human PRO polypeptide SEQ ID NO 294.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1362  
ID ADA82177 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1363  
ID ADA75140 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1364  
ID ADA85218 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1365  
ID ADA84666 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1366  
ID ABO17500 standard; protein; 915 AA.  
DE Human PRO polypeptide #7.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1367  
ID ADB29922 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1368  
ID ABO43295 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1368  
ID ADA80450 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1369  
ID ADA75692 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1370  
ID ADA46917 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1371  
ID ADB25213 standard; protein; 915 AA.  
DE Human PRO polypeptide SEQ ID NO 294.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1372  
ID ADA93389 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1373  
ID ADB26739 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1374  
ID ADB31026 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1375  
ID ADA60954 standard; protein; 915 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1376  
ID ADB24101 standard; protein; 915 AA.  
DE Human PRO polypeptide SEQ ID NO 294.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;

RESULT 1377  
ID ADA96430 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1378  
ID ADA81002 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1379  
ID ADA95878 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1380  
ID ADB26187 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1381  
ID ADB21672 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 6; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1382  
ID ADA77451 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1383  
ID ADB18191 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1384  
ID ADA86874 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1385  
ID ADA16494 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1386



ID ADA12923 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003049622-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1387  
 ID ADA1791 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003082540-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1388  
 ID ADA8797 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003082700-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1389  
 ID ADA46365 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003054516-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1390  
 ID ADA17138 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003017498-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1391  
 ID ADA42641 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003054351-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1392  
 ID ADB28395 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003082699-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1393  
 ID ADB28947 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003082706-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1394  
 ID ADA7689 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003059909-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1395  
 ID ADA88529 standard; protein; 915 AA.

DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003073213-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1396  
 ID ADA97534 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003082686-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1397  
 ID ADB27291 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003022239-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1398  
 ID ADB22224 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003087344-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1399  
 ID ABO17561 standard; protein; 915 AA.  
 DE Human PRO polypeptide #7.  
 PN US2003064923-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1400  
 ID ADA66915 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003068793-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1401  
 ID ADB22776 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003077711-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1402  
 ID ADB23549 standard; protein; 915 AA.  
 DE Human PRO polypeptide SEQ ID NO 294.  
 PN US2003077712-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1403  
 ID ADA92271 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003082712-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1404  
 ID ADB15334 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003087352-A1.  
 PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1405  
ID ADB38586 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1406  
ID ADB38034 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1407  
ID ADB66506 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1408  
ID ADB89586 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1409  
ID ADB90318 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1410  
ID ADB77560 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1411  
ID ADB39419 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1412  
ID ADB74696 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1413  
ID ADB47042 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1414  
ID ADB66649 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1415  
ID ADB77254 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1416  
ID ADB34411 standard; protein; 915 AA.  
DE Human PRO polypeptide SEQ ID NO 294.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1417  
ID ADB35515 standard; protein; 915 AA.  
DE Human PRO polypeptide SEQ ID NO 294.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1418  
ID ADB33859 standard; protein; 915 AA.  
DE Human PRO polypeptide SEQ ID NO 294.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1419  
ID ADB34963 standard; protein; 915 AA.  
DE Human PRO polypeptide SEQ ID NO 294.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1420  
ID ADB36067 standard; protein; 915 AA.  
DE Human PRO polypeptide SEQ ID NO 294.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1421  
ID ADB46462 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1422  
ID ADC28342 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1423  
ID ADC28342 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1423  
 ID ADC39542 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003059828-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1424  
 ID ADC40056 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003059829-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1425  
 ID ADC18864 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003036061-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1426  
 ID ADC34180 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003036094-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1427  
 ID ADC29235 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003049676-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1428  
 ID ADC28766 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003049677-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1429  
 ID ADC40651 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003054400-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1430  
 ID ADC19308 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003054441-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1431  
 ID ADC33756 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003073077-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1432

RESULT 1432  
 ID ADC12826 standard; protein; 915 AA.  
 DE Human secreted/transmembrane protein, #8.  
 PN US2003073079-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1433  
 ID ADC50335 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003092106-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1434  
 ID ADC71882 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003092107-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1435  
 ID ADC59861 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003092105-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1436  
 ID ADC52868 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein Seq ID294.  
 PN US2003087365-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1437  
 ID ADC57222 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein Seq ID294.  
 PN US2003087366-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1438  
 ID ADC60413 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003087367-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1439  
 ID ADC50888 standard; protein; 915 AA.  
 DE Novel human secreted and transmembrane protein PRO219.  
 PN US2003087361-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1440  
 ID ADC65415 standard; protein; 915 AA.  
 DE Human PRO polypeptide #147.  
 PN US2003087362-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.6%; Score 370; DB 7; Length 915;  
 Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
 RESULT 1441

ID ADC54513 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein Seq ID294.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1442  
ID ADC53474 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein Seq ID294.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1443  
ID ADC58997 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein Seq ID294.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1444  
ID ADC55875 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein Seq ID294.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1445  
ID ADC58445 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein Seq ID294.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1446  
ID ADC12378 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1447  
ID ADD03119 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1448  
ID ADC90111 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1449  
ID ADC69530 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1450  
ID ADC48419 standard; protein; 915 AA.

DE Human PRO polypeptide #147.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1451  
ID ADD09948 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1452  
ID ADD04523 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1453  
ID ADC80479 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1454  
ID ADD10986 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1455  
ID ADC47867 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1456  
ID ADD04833 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1457  
ID ADC79927 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1458  
ID ADD09396 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1459  
ID ADD03839 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.

PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1460  
ID ADD03415 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1461  
ID ADD41109 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1462  
ID ADD52248 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1463  
ID ADD52988 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1464  
ID ADD53540 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1465  
ID ADD51696 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1466  
ID ADD02495 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1467  
ID ADD01929 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1468  
ID ADD54111 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003203432-A1.

PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1469  
ID ADD92428 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1470  
ID ADD91324 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1471  
ID ADE03938 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1472  
ID ADE32235 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1473  
ID ADE22167 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1474  
ID ADD79391 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1475  
ID ADE41927 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1476  
ID ADE17744 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1477  
ID ADD91876 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199053-A1.  
PD 23-OCT-2003.

PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1478  
ID ADE3339 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1479  
ID ADE33891 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1480  
ID ADD79943 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1481  
ID ADD92980 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1482  
ID ADE19400 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1483  
ID ADE34667 standard; protein; 915 AA.  
DE Human secreted/transmembrane protein, #8.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1484  
ID ADE18848 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1485  
ID ADE43044 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1486  
ID ADD95833 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003198059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;

Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1487  
ID ADE22719 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1488  
ID ADD78837 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1489  
ID ADE32787 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1490  
ID ADE42479 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1491  
ID ADD80495 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1492  
ID ADD89523 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1493  
ID ADE40807 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1494  
ID ADE04606 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;  
Query Match  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1495  
ID ADE92735 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. 10.6%; Score 370; DB 7; Length 915;

Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1496  
ID ADG21444 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1497  
ID ADG23085 standard; protein; 915 AA.  
DE Novel human secreted and transmembrane protein PRO219.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1498  
ID ADF97420 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1499  
ID ADG80484 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;  
RESULT 1500  
ID ADG79932 standard; protein; 915 AA.  
DE Human PRO polypeptide #147.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.6%; Score 370; DB 7; Length 915;  
Best Local Similarity 17.9%; Pred. No. 2.5e-23;

**THIS PAGE BLANK (USPTO)**